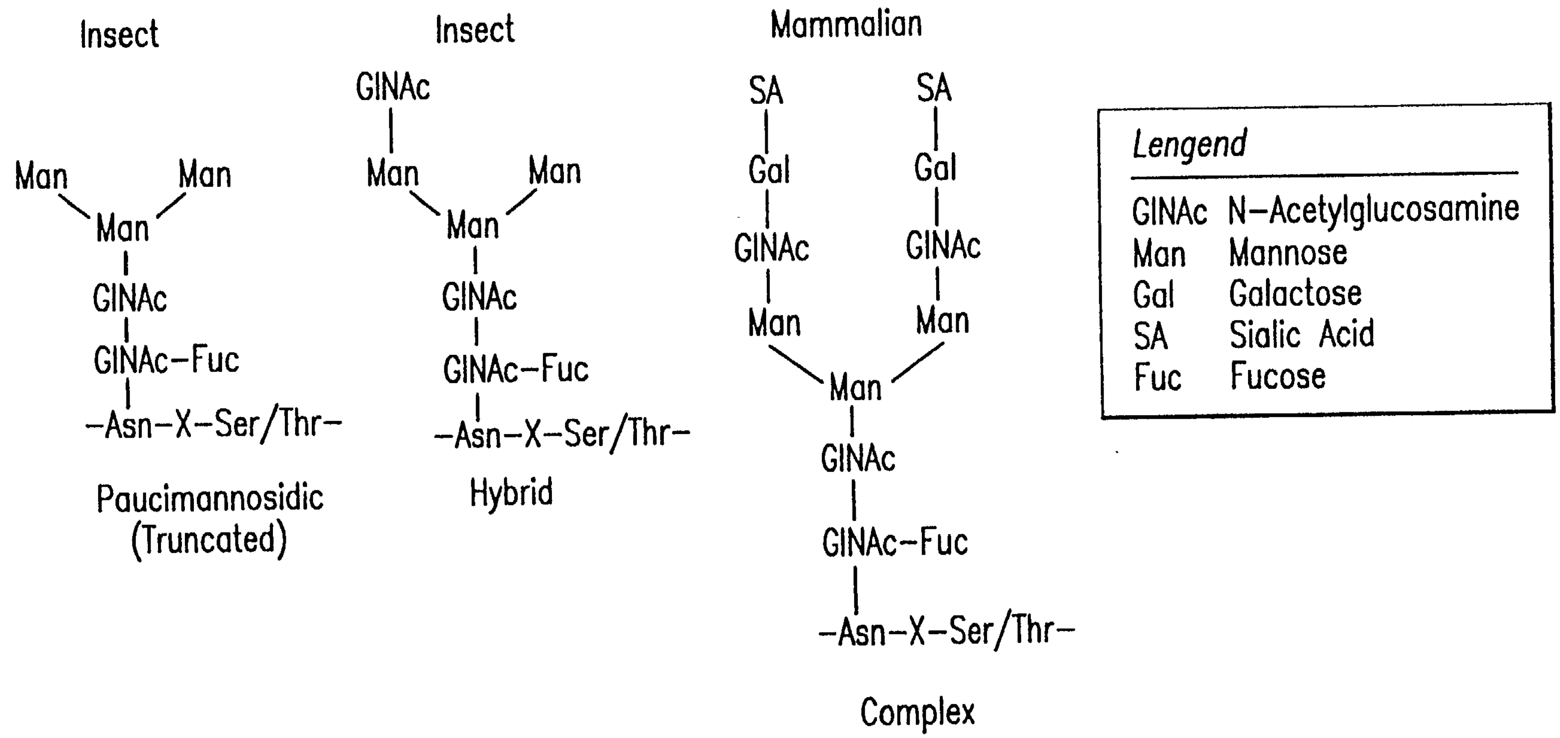

Insect
Man
Man
Man
GlNAc
GlNAc–Fuc
–Asn–X–Ser/Thr–
Paucimannosidic
(Truncated)
Insect
GlNAc
Man
Man
Man
GlNAc
GlNAc–Fuc
–Asn–X–Ser/Thr–
Hybrid
Mammalian
SA
SA
Gal
Gal
GlNAc
GlNAc
Man
Man
Man
GlNAc
GlNAc–Fuc
–Asn–X–Ser/Thr–
Complex
Lengend
GlNAc N–Acetylglucosamine
Man Mannose
Gal Galactose
SA Sialic Acid
Fuc Fucose

FIG.1

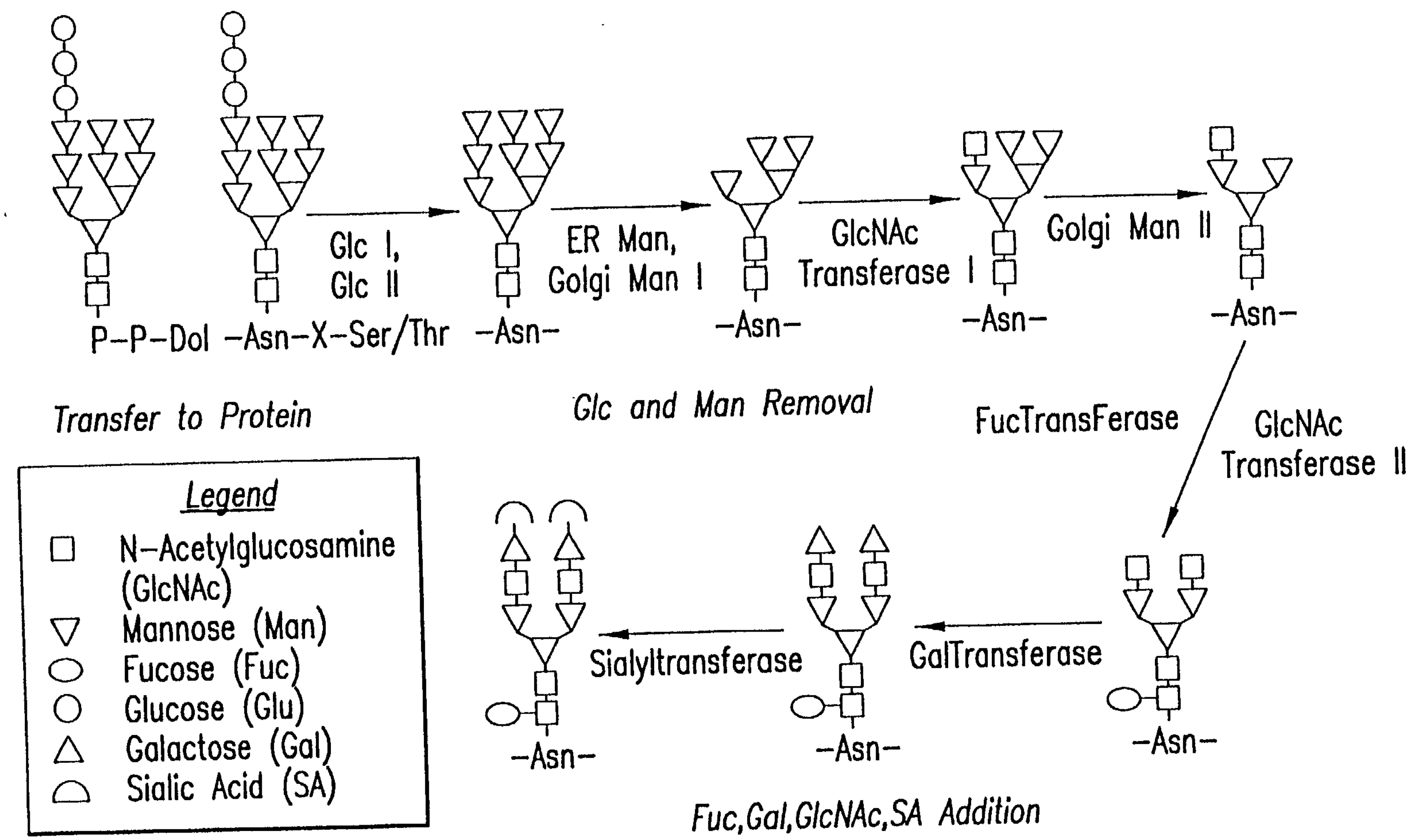

P–P–Dol
–Asn–X–Ser/Thr
Glc I,
Glc II
–Asn–
ER Man,
Golgi Man I
–Asn–
GlcNAc
Transferase I
–Asn–
Golgi Man II
–Asn–
Transfer to Protein
Glc and Man Removal
FucTransFerase
GlcNAc
Transferase II
–Asn–
GalTransferase
–Asn–
Sialyltransferase
–Asn–
Fuc,Gal,GlcNAc,SA Addition
Legend
N–Acetylglucosamine
(GlcNAc)
Mannose (Man)
Fucose (Fuc)
Glucose (Glu)
Galactose (Gal)
Sialic Acid (SA)

FIG.2

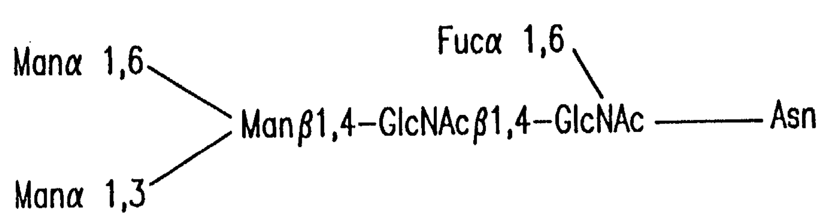


FIG.3

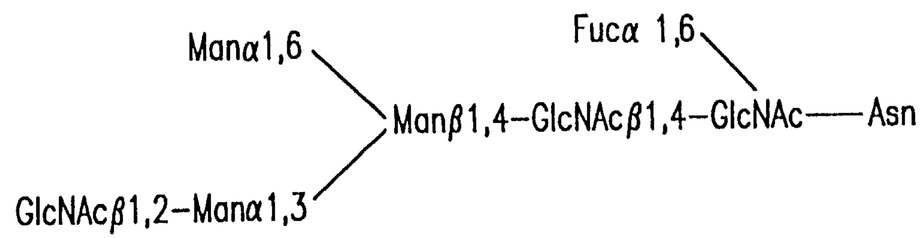


FIG.4A

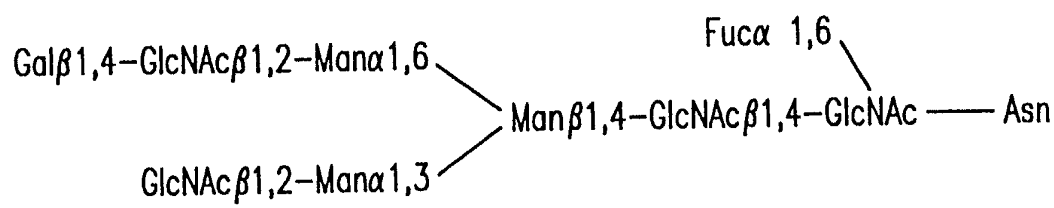


FIG.4B

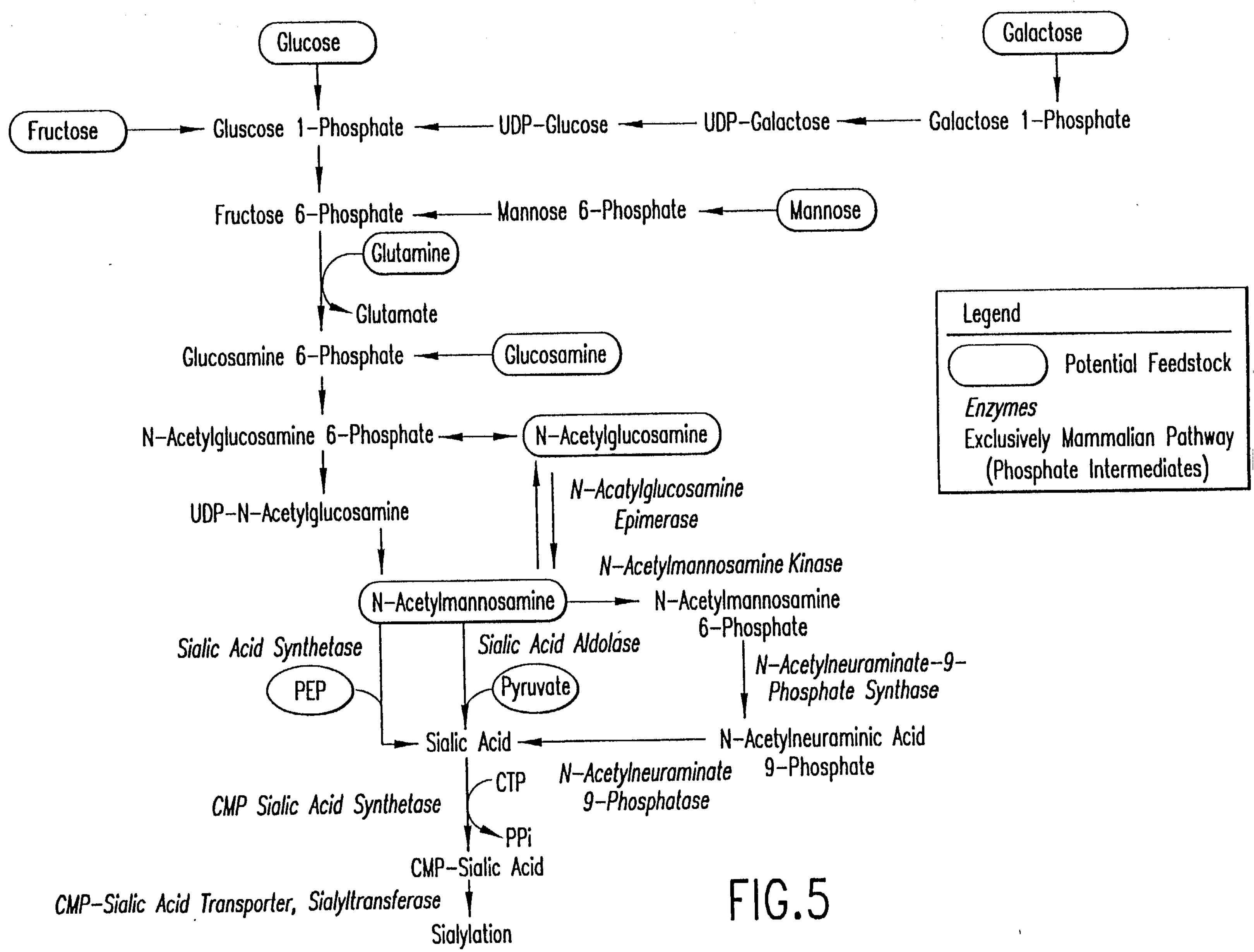
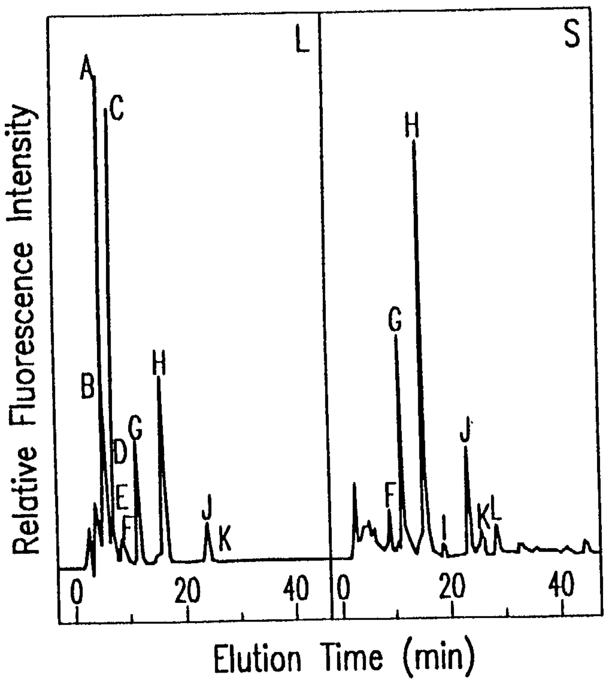
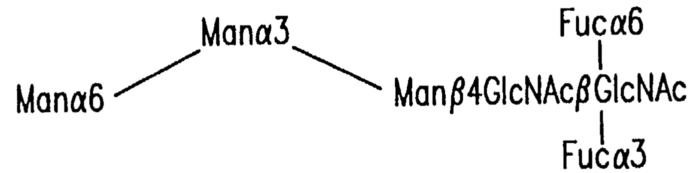

Glucose
Galactose
Fructose
Gluscose 1-Phosphate
UDP-Glucose
UDP-Galactose
Galactose 1-Phosphate
Fructose 6-Phosphate
Mannose 6-Phosphate
Mannose
Glutamine
Glutamate
Glucosamine 6-Phosphate
Glucosamine
N-Acetylglucosamine 6-Phosphate
N-Acetylglucosamine
UDP-N-Acetylglucosamine
N-Acatylglucosamine Epimerase
N-Acetylmannosamine Kinase
N-Acetylmannosamine
N-Acetylmannosamine 6-Phosphate
Sialic Acid Synthetase
Sialic Acid Aldolase
PEP
Pyruvate
N-Acetylneuraminate-9-Phosphate Synthase
Sialic Acid
N-Acetylneuraminic Acid 9-Phosphate
N-Acetylneuraminate 9-Phosphatase
CTP
PPi
CMP Sialic Acid Synthetase
CMP-Sialic Acid
CMP-Sialic Acid Transporter, Sialyltransferase
Sialylation
Legend
Potential Feedstock
Enzymes
Exclusively Mammalian Pathway (Phosphate Intermediates)

FIG.5



L
S
A
B
C
D
E
F
G
H
J
K
I
L
0
20
40
Relative Fluorescence Intensity
Elution Time (min)

FIG.6



Manα6
Manα3
Manβ4GlcNAcβGlcNAc
Fucα6
Fucα3

FIG.7

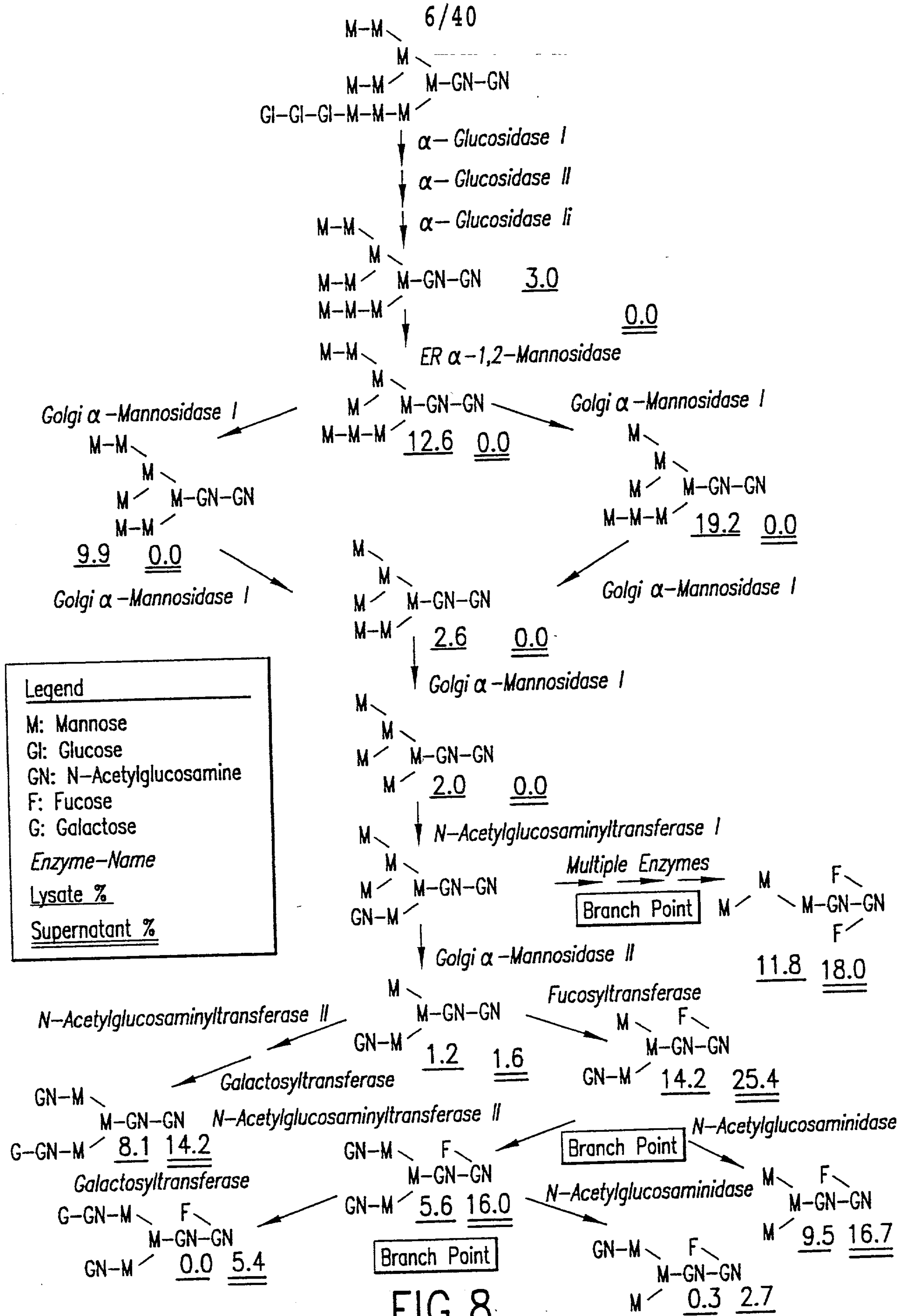

α– Glucosidase I
α– Glucosidase II
α– Glucosidase Ii
ER α-1,2-Mannosidase
Golgi α -Mannosidase I
Golgi α -Mannosidase I
Golgi α -Mannosidase I
Golgi α-Mannosidase I
Golgi α -Mannosidase I
N–Acetylglucosaminyltransferase I
Multiple Enzymes
Branch Point
Golgi α -Mannosidase II
Fucosyltransferase
N–Acetylglucosaminyltransferase II
Galactosyltransferase
N–Acetylglucosaminyltransferase II
Branch Point
N–Acetylglucosaminidase
Galactosyltransferase
N–Acetylglucosaminidase
Branch Point
3.0
0.0
12.6 0.0
9.9 0.0
19.2 0.0
2.6 0.0
2.0 0.0
11.8 18.0
1.2 1.6
14.2 25.4
8.1 14.2
5.6 16.0
9.5 16.7
0.0 5.4
0.3 2.7
Legend
M: Mannose
Gl: Glucose
GN: N–Acetylglucosamine
F: Fucose
G: Galactose
Enzyme–Name
Lysate %
Supernatant %

FIG.8

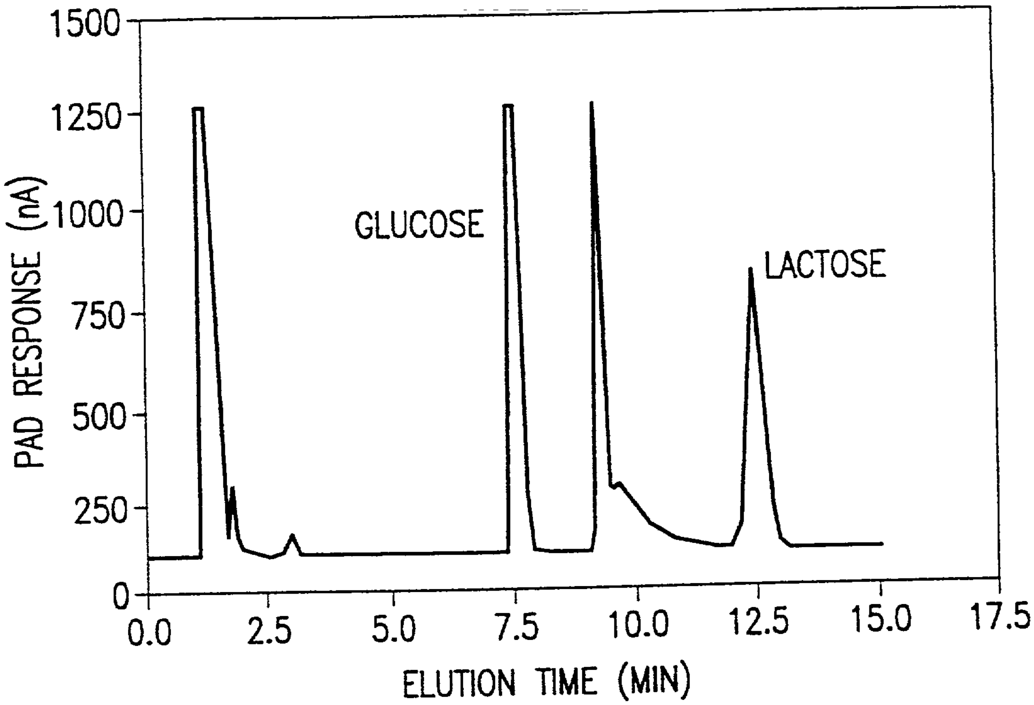

PAD RESPONSE (nA)
GLUCOSE
LACTOSE
ELUTION TIME (MIN)

FIG. 9

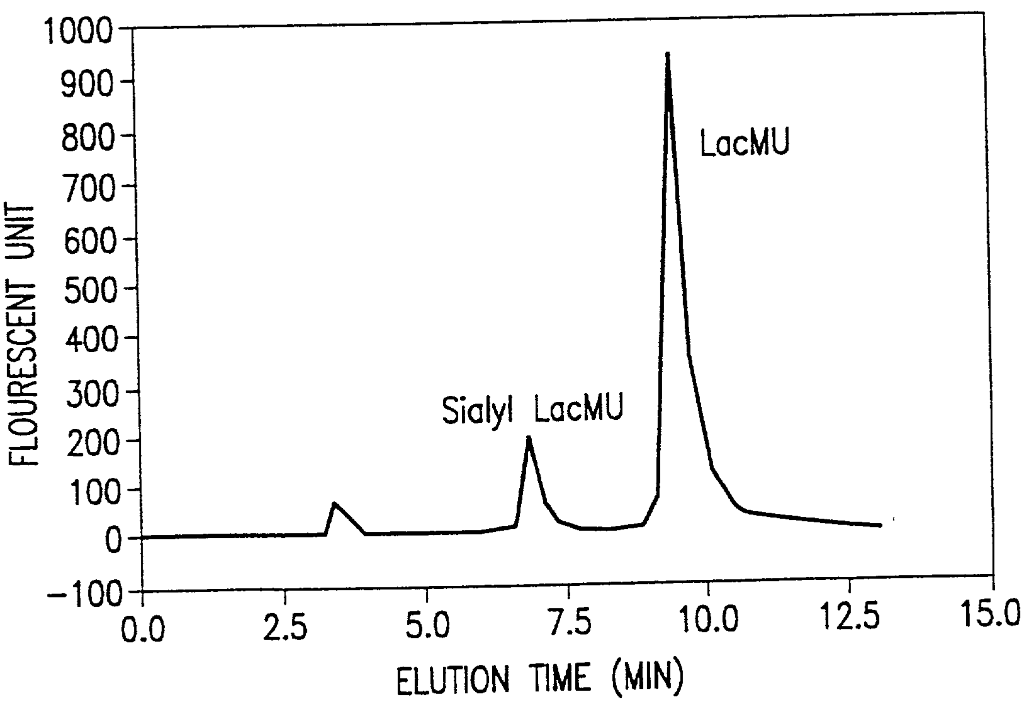
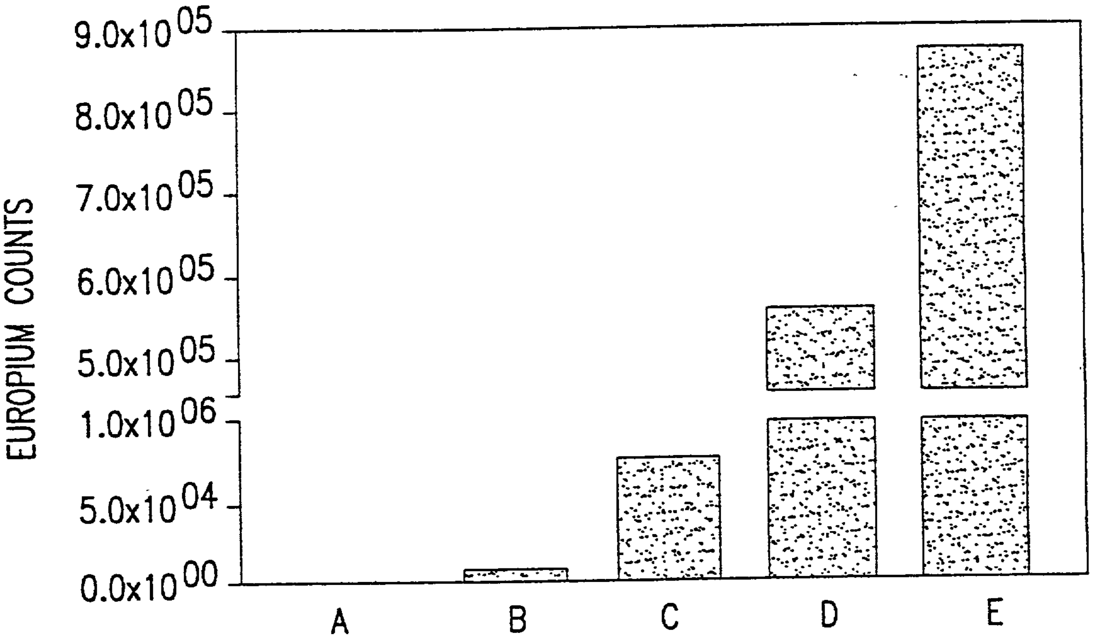

FLOURESCENT UNIT
Sialyl LacMU
LacMU
ELUTION TIME (MIN)

FIG. 10



EUROPIUM COUNTS
9.0x10 05
8.0x10 05
7.0x10 05
6.0x10 05
5.0x10 05
1.0x10 06
5.0x10 04
0.0x10 00
A
B
C
D
E

FIG. 11

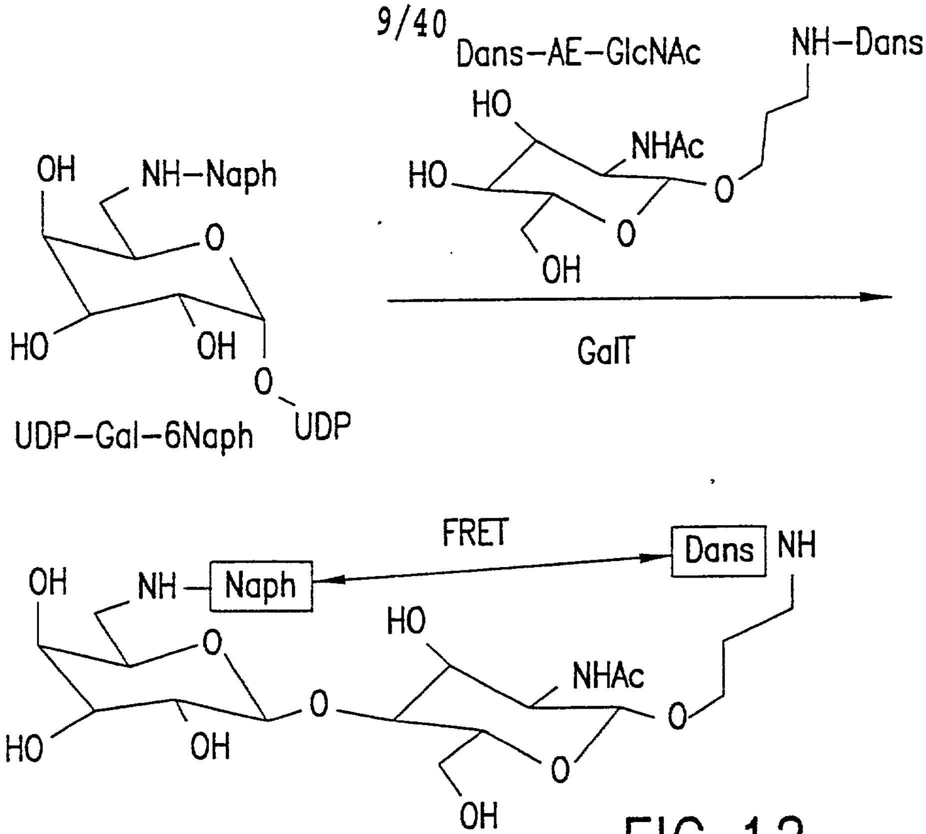

Dans–AE–GlcNAc
NH–Dans
HO
NHAc
HO
O
O
OH
OH
NH–Naph
O
HO
OH
O
UDP
UDP–Gal–6Naph
GalT
FRET
Dans
NH
OH
NH–
Naph
HO
O
NHAc
O
O
HO
OH
O
OH

FIG. 12

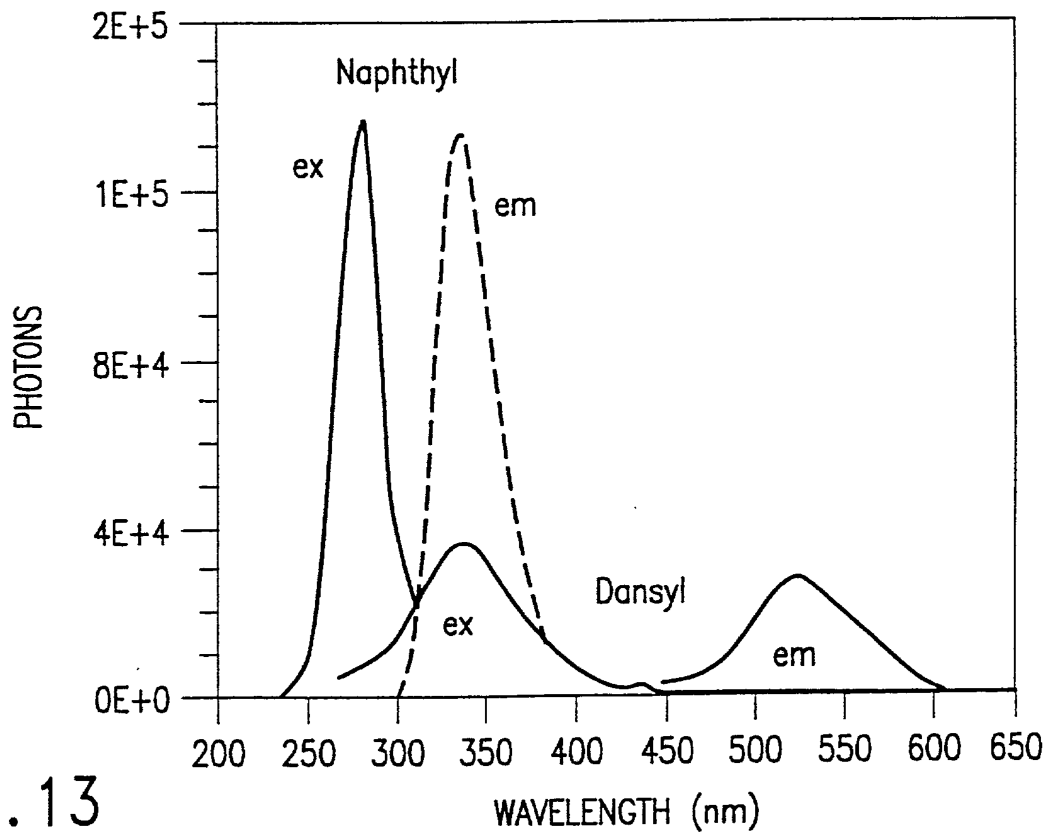
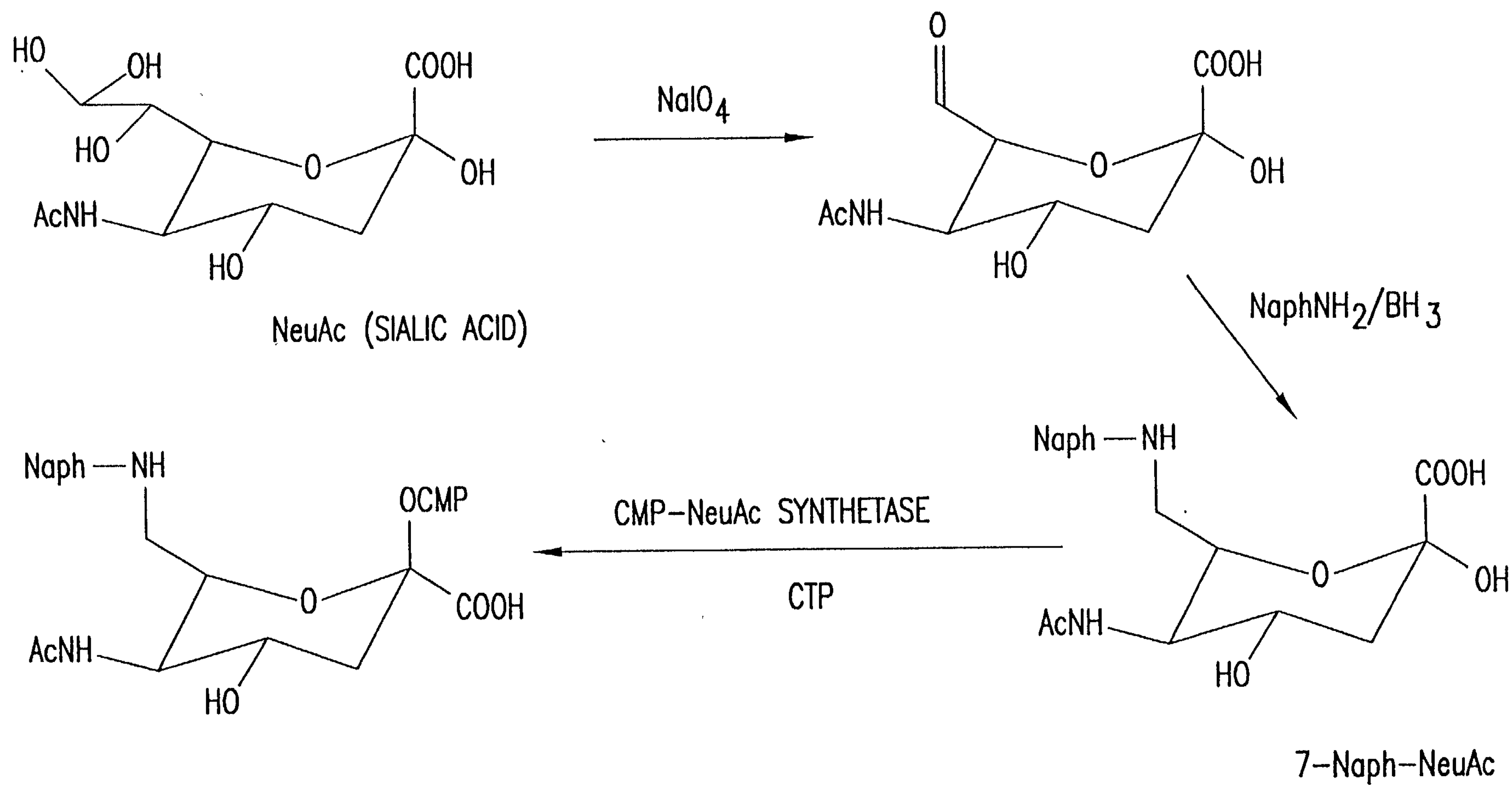

2E+5
1E+5
8E+4
4E+4
0E+0
PHOTONS
Naphthyl
ex
em
Dansyl
ex
em
200
250
300
350
400
450
500
550
600
650
WAVELENGTH (nm)

FIG. 13



HO
OH
HO
COOH
OH
AcNH
O
HO
NeuAc (SIALIC ACID)
NaIO4
O
COOH
OH
AcNH
O
HO
NaphNH2/BH3
Naph — NH
COOH
O
OH
AcNH
HO
7-Naph-NeuAc
CMP-NeuAc SYNTHETASE
CTP
Naph — NH
OCMP
O
COOH
AcNH
HO

FIG. 14

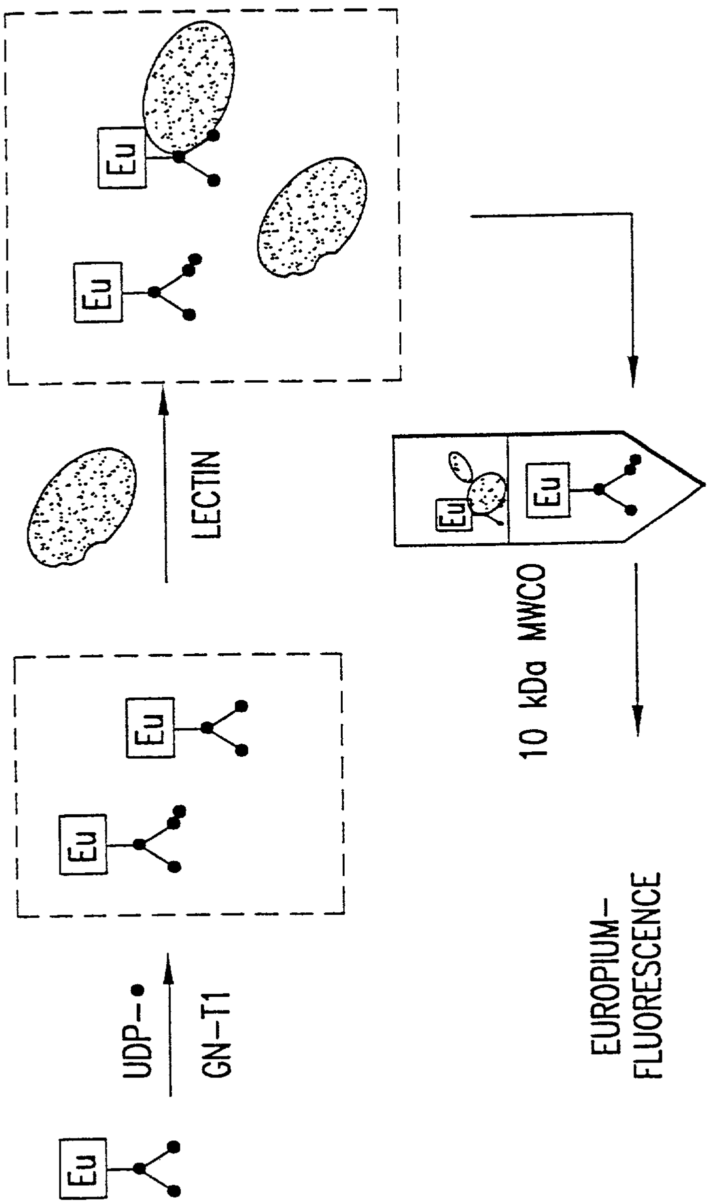


FIG. 15

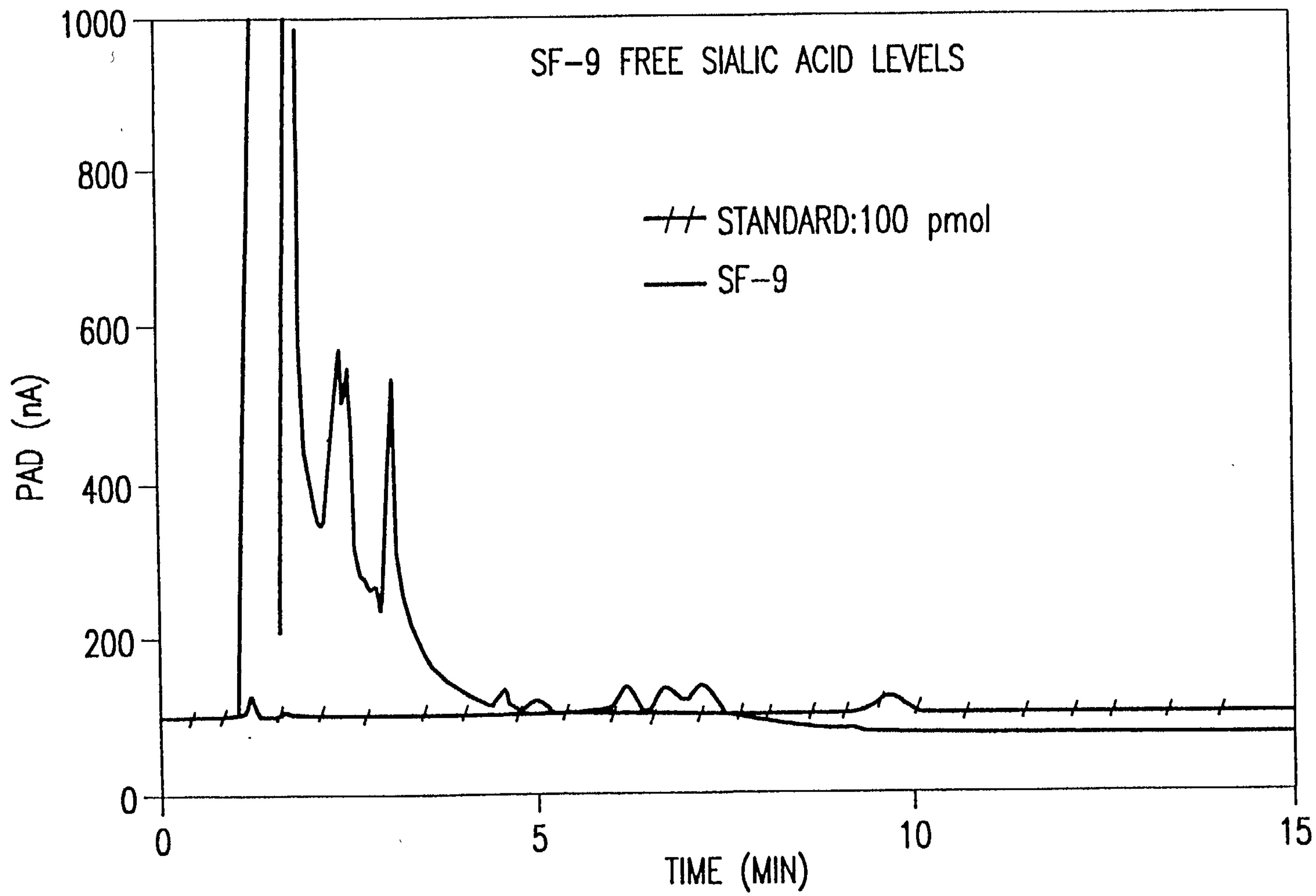

SF-9 FREE SIALIC ACID LEVELS
STANDARD:100 pmol
SF-9
PAD (nA)
1000
800
600
400
200
0
0
5
10
15
TIME (MIN)

FIG.16A

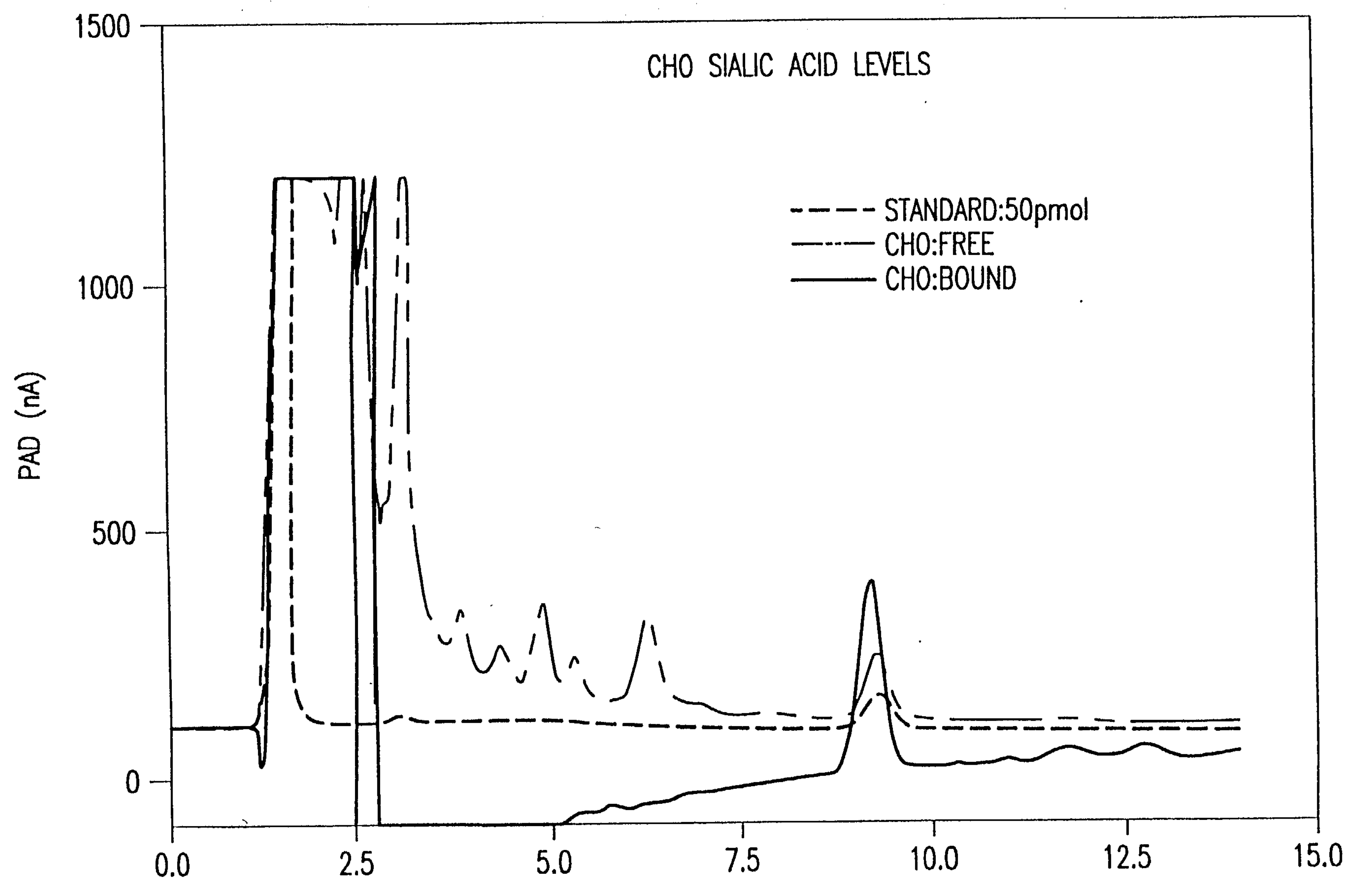

CHO SIALIC ACID LEVELS
STANDARD:50pmol
CHO:FREE
CHO:BOUND
PAD (nA)
1500
1000
500
0
0.0
2.5
5.0
7.5
10.0
12.5
15.0
TIME (MIN)

FIG.16B

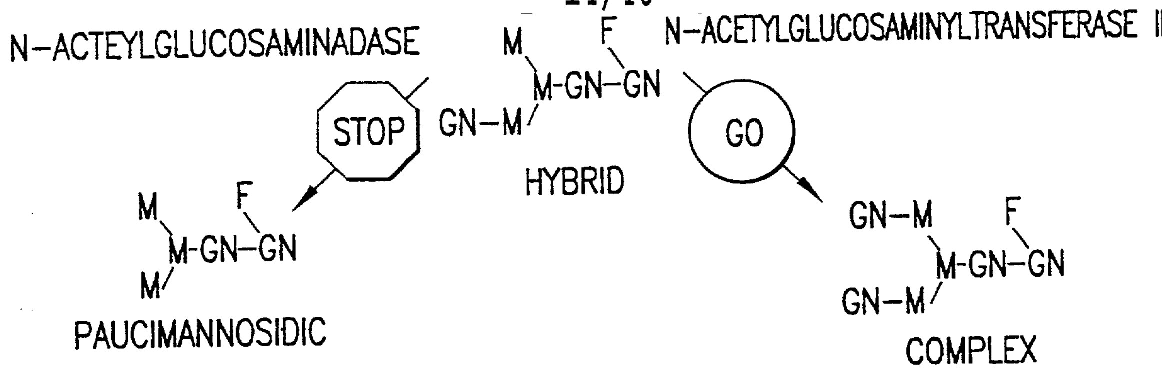
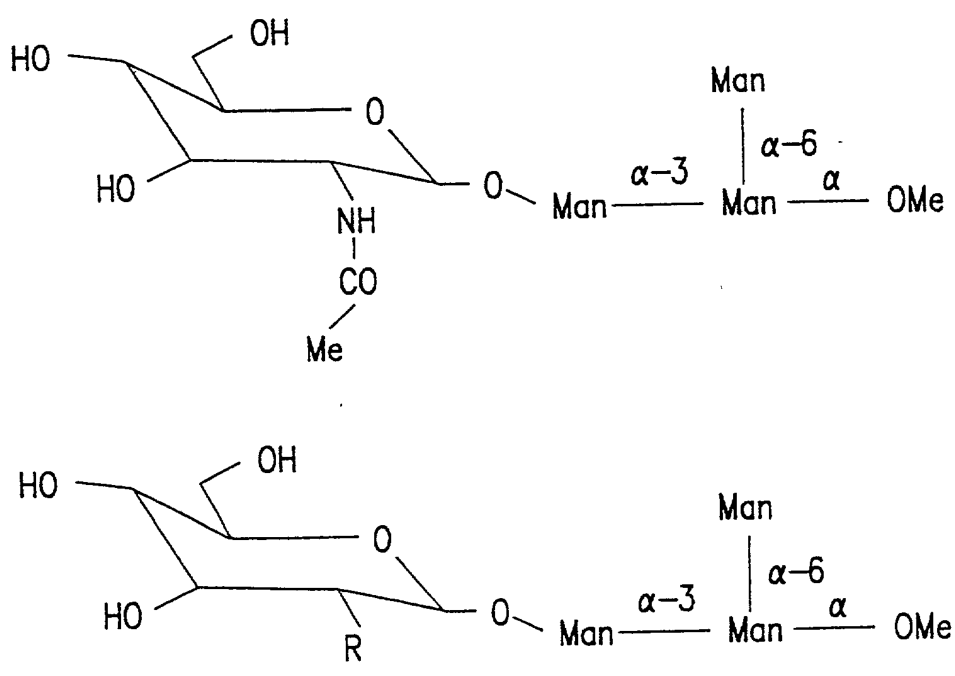


FIG. 17



R=MeCONH I I
R=BrCH$_2$CONH III
R=N$_2$CH$_2$CONH IV

FIG. 19

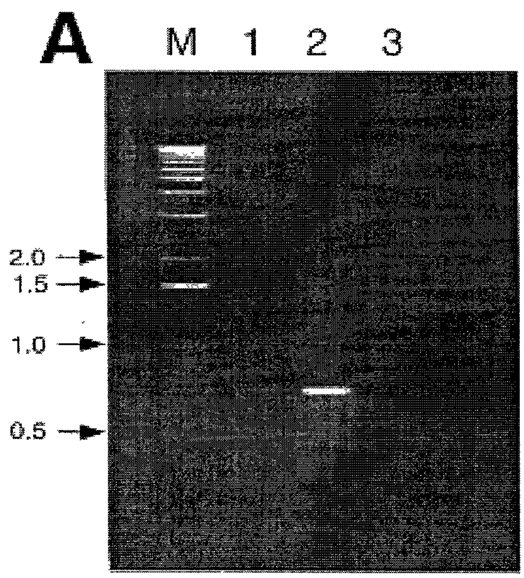


FIG. 18A

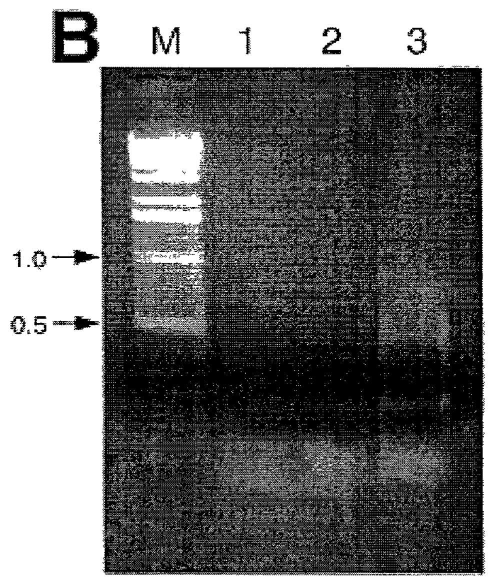


FIG. 18B

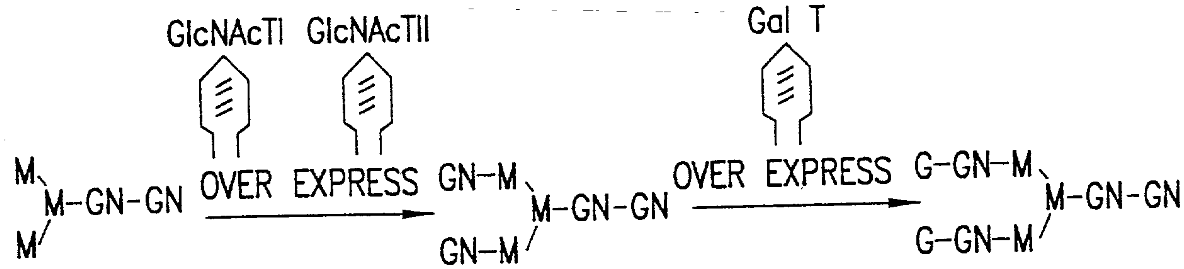


FIG. 20

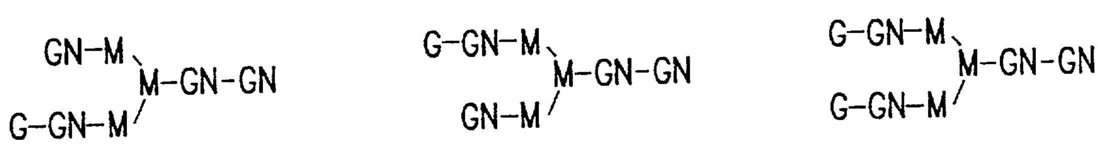
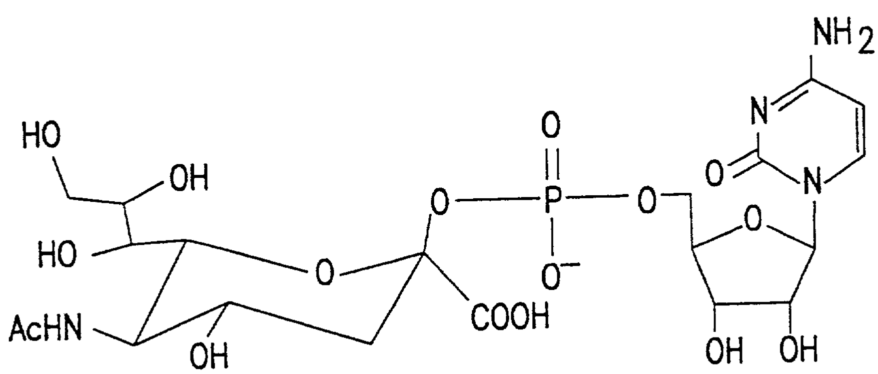


FIG. 21



CMP-SIALIC ACID

FIG. 22

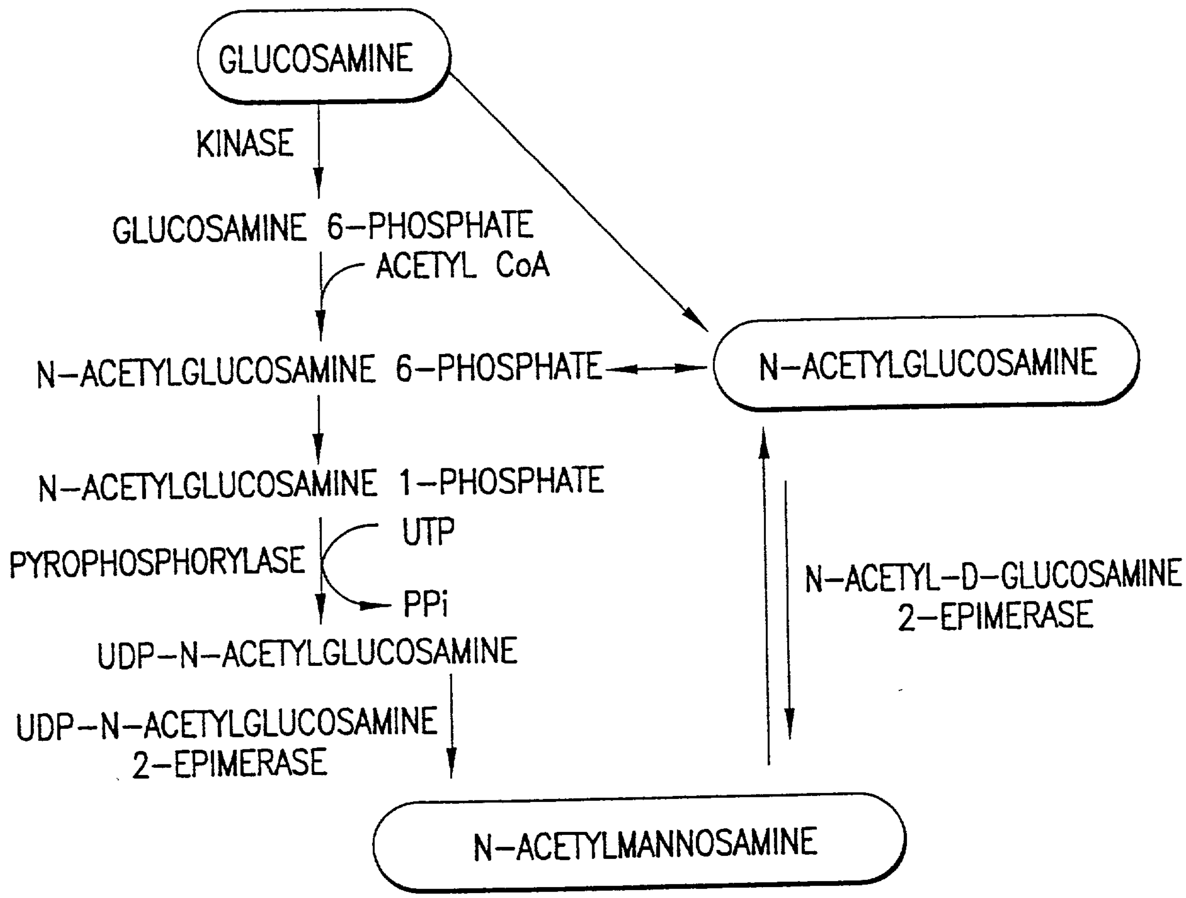

GLUCOSAMINE
KINASE
GLUCOSAMINE 6-PHOSPHATE
ACETYL CoA
N-ACETYLGLUCOSAMINE 6-PHOSPHATE
N-ACETYLGLUCOSAMINE
N-ACETYLGLUCOSAMINE 1-PHOSPHATE
UTP
PYROPHOSPHORYLASE
PPi
UDP-N-ACETYLGLUCOSAMINE
UDP-N-ACETYLGLUCOSAMINE
2-EPIMERASE
N-ACETYL-D-GLUCOSAMINE
2-EPIMERASE
N-ACETYLMANNOSAMINE

FIG. 23

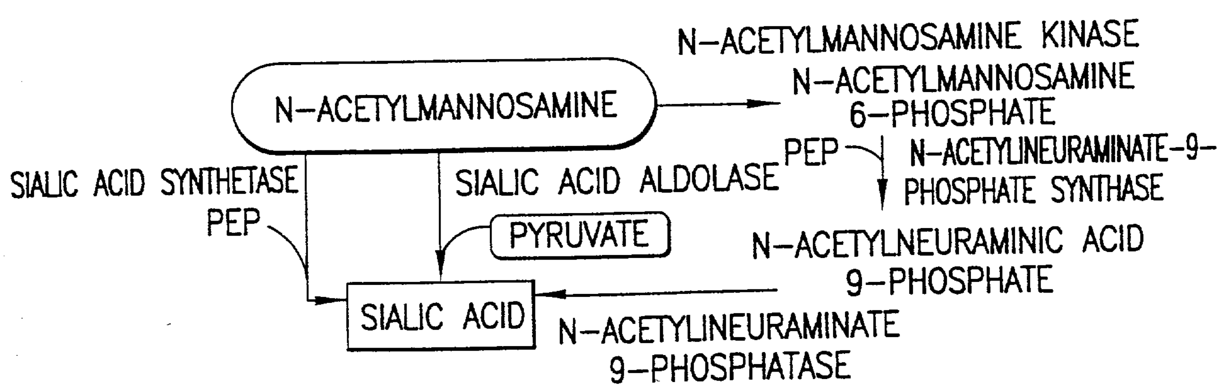

N-ACETYLMANNOSAMINE KINASE
N-ACETYLMANNOSAMINE
N-ACETYLMANNOSAMINE
6-PHOSPHATE
PEP
N-ACETYLNEURAMINATE-9-
PHOSPHATE SYNTHASE
SIALIC ACID SYNTHETASE
PEP
SIALIC ACID ALDOLASE
PYRUVATE
N-ACETYLNEURAMINIC ACID
9-PHOSPHATE
SIALIC ACID
N-ACETYLINEURAMINATE
9-PHOSPHATASE

FIG. 24

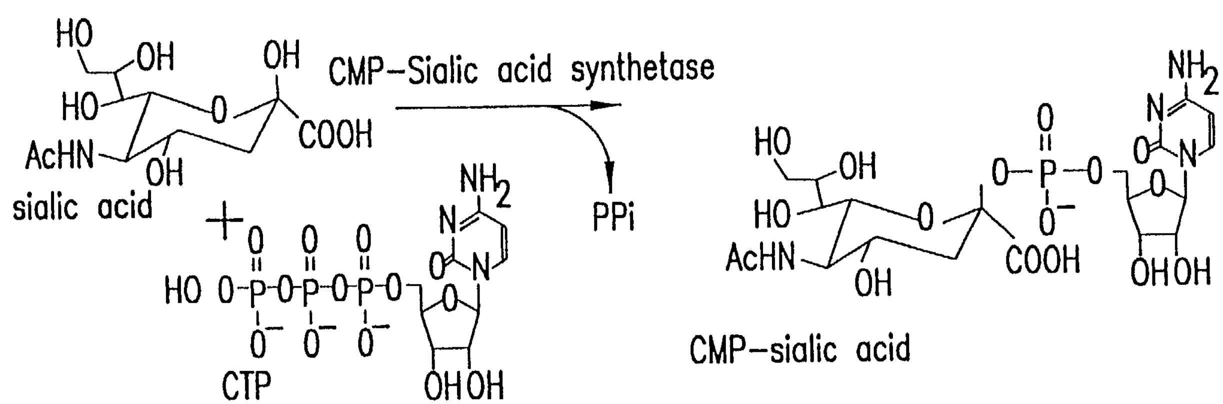

CMP–Sialic acid synthetase
PPi
sialic acid
CTP
CMP–sialic acid

FIG.25

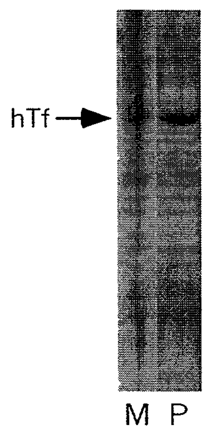


FIG. 26

ATGGCCTTCCCAAAGAAGAAACTTCAGGGTCTTGTGGCTGCAACCATCACGCCAATGACTGAGAATGGAGAAATCAA
CTTTTCAGTAATTGGTCAGTATGTGGATTATCTTGTGAAAGAACAGGGAGTGAAGAACATTTTTGTGAATGGCACAA
CAGGAGAAGGCCTGTCCCTGAGCGTCTCAGAGCGTCGCCAGGTTGCAGAGGAGTGGGTGACAAAAGGGAAGGACAAG
CTGGATCAGGTGATAATTCACGTAGGAGCACTGAGCTTGAAGGAGTCACAGGAACTGGCCCAACATGCAGCAGAAAT
AGGAGCTGATGGCATCGCTGTCATTGCACCGTTCTTCCTCAAGCCATGGACCAAAGATATCCTGATTAATTTCCTAA
AGGAAGTGGCTGCTGCCGCCCCTGCCCTGCCATTTTATTACTATCACATTCCTGCCTTGACAGGGGTAAAGATTCGT
GCTGAGGAGTTGTTGGATGGGATTCTGGATAAGATCCCCACCTTCCAAGGGCTGAAATTCAGTGATACAGATCTCTT
AGACTTCGGGCAATGTGTTGATCAGAATCGCCAGCAACAGTTTGCTTTCCTTTTTGGGGTGGATGAGCAACTGTTGA
GTGCTCTGGTGATGGGAGCAACTGGAGCAGTGGGCAGTTTTGTATCCAGAGATTTATCAACTTTGTTGTCAAACTAG
GTTTTGGAGTGTCACAGACCAAAGCCATCATGACTCTGGTCTCTGGGATTCCAATGGGCCCACCCCGGCTTCCACTG
CAGAAAGCCTCCAGGGAGTTTACTGATAGTGCTGAAGCTAAACTGAAGAGCCTGGATTTCCTTTCTTTCACTGATTT
AAAGGATGGAAACTTGGAAGCTGGTAGCTAGTGCCTCTCTATCAAATCAGGGTTTGCACCTTGAGACATAATCTACC
TTAAATAGTGCATTTTTTTCTCAGGGAATTTTAGATGAACTTGAATAAACTCTCCTAGCAAATGAAATCTCACAATA
AGCATTGAGGTACCTTTTGTGAGCCTTAAAAAGTCTTATTTTGTGAAGGGGCAAAAACTCTAGGAGTCACAACTCTC
AGTCATTCATTTCACAGATTTTTTTGTGGAGAAATTTCTGTTTATATGGATGAAATGGAATCAAGAGGAAAATTGTA
ATTGATTAATTCCATCTGTCTTTAGGAGCTCTCATTATCTCGGTCTCTGGTTCCTAATCCTATTTTAAAGTTGTCTA
ATTTTAAACCACTATAATATGTCTTCATTTTAATAAATATTCATTTGGAATCTAGGAAAACTCTGAGCTACTGCATT
TAGGCAGGCACTTTAATACCAAACTGTAACATGTCTCAACTGTATACAACTCAAAATACACCAGCTCATTTGGCTGC
TCAGTCTAACTCTAGAATGGATGCTTTTGAATTCATTTCGATG

FIG.27

MAFPKKKLQGLVAATITPMTENGEINFSVIGQYVDYLVKEQGVKNIFVNGTTGEGLSLSVSERRQVAEEWVTKGKDKLDQ
VIIHVGALSLKESQELAQHAAEIGADGIAVIAPFFLKPWTKDILINFLKEVAAAAPALPFYYYHIPALTGVKIRAEELLD
GILDKIPTFQGLKFSDTDLLDFGQCVDQNRQQQFAFLFGVDEQLLSALVMGATGAVGSFVSRDLSTLLSN.VLECHRPKP
S.LWSLGFQWAHPGFHCRKPPGSLLIVLKLN.RAWISFLSLI.RMETWKLVASASLSNQGFAPLRHNL

FIG.28

ATGGACTCGGTGGAGAAGGGGGCCGCCACCTCCGTCTCCAACCCGCGGGGCGACCGTCCCGGGCCGGCCGCCGAAGCT
GCAGCGCAACTCTCGCGGCGGCCAGGGCCGAGGTGTGGAGAAGCCCCCGCACCTGGCAGCCCTAATTCTGGCCCGGGAG
GCAGCAAAGGCATCCCCCTGAAGAACATTAAGCACCTGGCGGGGGTCCCGCTCATTGGCTGGGTCCTGCGTGCGGCCCTG
GATTCAGGGGCCTTCCAGAGTGTATGGGTTTCGACAGACCATGATGAAATTGAGAATGTGGCCAAACAATTTGGTGCACA
AGTTCATCGAAGAAGTTCTGAAGTTTCAAAAGACAGCTCTACCTCACTAGATGCCATCATAGAATTTCTTAATTATYATA
ATGAGGKTGACATTGTAGGAAATATTCAAGCTACTTCTYCATGTTTACATCCTACTGATCTTCAAAAAGTTGCAGAAATG
ATTCGAGAAGAAGGATATGATTCTGKTTTCTCTGTTGTGAGACGCCATCAGTTTCGATGGAGTGAAATTCAGAAAGGAGT
TCGTGAAGTGACCGAACCTCTGAATTTAAATCCAGCTAAACGGCCTCGTCGACAAGACTGGGATGGAGAATTATATGAAA
ATGGCTCATTTTATTTTGCTAAAAGACATTTGATAGAGATGGGTTACTTGCAGGGTGGAAAATGGCATACTACGAAATGC
GAGCTGGAACATAGTGTGGATATAGATGTGGATATTGATTGGCCTATTGCAGAGCAAAGAGTATTAAGATATGGCTATTT
TGGCAAAGAGAAGCTTAAGGAAATAAAACTTTTGGTTTGCAATATTGATGGATGTCTCACCAATGGCCACATTTATGTAT
CAGGAGACCAAAAAGAAATAATATCTTATGATGTAAAAGATGCTATTGGGATAAGTTTATTAAAGAAAAGTGGTATTGAG
GTGAGGCTAATCTCAGAAAGGGCCTGTTCAAAGCAGACGCTGTCTTCTTTAAAACTGGATTGCAAAATGGAAGTCAGTGT
ATCAGACAAGCTAGCAGTTGTAGATGAATGGAGAAAAGAAATGGGCCTGTGCTGGAAAGAAGTGGCATATCTTGGAAATG
AAGTGTCTGATGAAGAGTGCTTGAAGAGAGTGGGCCTAAGTGGCGCTCCTGCTGATGCCTGTTCCTACGCCCAGAAGGCT
GTTGGATACATTTGCAAATGTAATGGTGGCCGTGGTGCCATCCGAGAATTTGCAGAGCACATTTGCCTACTAATGGAAAA
AGTTAATAATTCATGCCAAAAATAG

FIG.29

MDSVEKGAATSVSNPRGRPSRGRPPKLQRNSRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGWVLRAAL
DSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKDSSTSLDAIIEFLNYXNEXDIVGNIQATSXCLHPTDLQKVAEM
IREEGYDSXFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQDWDGELYENGSFYFAKRHLIEMGYLQGGKWHTTKC
ELEHSVDIDVDIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVSGDQKEIISYDVKDAIGISLLKKSGIE
VRLISERACSKQTLSSLKLDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLKRVGLSGAPADACSYAQKA
VGYICKCNGGRGAIREFAEHICLLMEKVNNSCQK.

FIG.30

ATGCCGCTGGAGCTGGAGCTGTGTCCCGGGCGCTGGGTGGCGGGCAACACCCGTGCTTCATCATTGCCGAGATCGGCCA
GAACCACCAGGGCGACCTGGACGTAGCCAAGCGCATGATCCGCATGGCCAAGGAGTGTGGGGCTGATTGTGCCAAGTTCC
AGAAGAGTGAGCTAGAATTCAAGTTTAATCGGAAAGCCTTGGAGAGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG
TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGGTACGCCGAGGAGGTTGGGAT
CTTCTTCACTGCCTCTGGCATGGATGAGATGGCAGTTGAATTCCTGCATGAACTGAATGTTCCATTTTTCAAAGTTGGAT
CTGGAGACACTAATAATTTTCCTTATCTGGAAAAGACAGCCAAAAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAG
TCAATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGCTTCTTGCAGTGTACCAGCGC
ATACCCGCTCCAGCCTGAGGACGTCAACCTGCGGGTCATCTCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGT
ATTCTGGGCATGAAACAGGCATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCAAGGTGTTGGAACGTCACATAACT
TTGGACAAGACCTGGAAGGGGAGTGACCACTCGGCCTCGCTGGAGCCTGGAGAACTGGCCGAGCTGGTGCGGTCAGTGCG
TCTTGTGGAGCGTGCCCTGGGCTCCCCAACCAAGCAGCTGCTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCAAGT
CTGTGGTGGCCAAAGTGAAAATTCCGGAAGGCACCATTCTAACAATGGACATGCTCACCGTGAAGGTGGGTGAGCCCAAA
GCCTATCCTCCTGAAGACATCTTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAAGAGGATGACACCATCATGGA
AGAATTGGTAGATAATCATGGCAAAAAAATCAAGTCTTAA

FIG.31

MPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVAKRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHELNVPFFKVGSGDTNNFPYLEKTAKKGRPMVISSGMQ
SMDTMKQVYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIPIGYSGHETGIAISVAAVALGAKVLERHIT
LDKTWKGSDHSASLEPGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKVKIPEGTILTMDMLTVKVGEPK
AYPPEDIFNLVGKKVLVTVEEDDTIMEELVDNHGKKIKS

FIG.32

Peak/code (G.U. ODS, amide)	PA–oligosaccharide structure	Secreted hTf (mol%) −GalT	+GalT
A/M8.1 (4.9,9.0)	Mana2–Mana6 Mana6 Mana3 Manb4–GlcNAcb4–GlcNAc Mana2–Mana2–Mana3	3.9	10.1
B1/M7.2 (5.1,8.1)	Mana2–Mana6 Mana6 Mana3 Manb4–GlcNAcb4–GlcNAc Mana2–Mana3	2.3	5.5
B2/M9.1 (5.2,9.7)	Mana2–Mana6 Mana6 Mana2–Mana3 Manb4–GlcNAcb4–GlcNAc Mana2–Mana2–Mana3	11.6	23.5
C/M7.1 (5.8,8.0)	Mana6 Mana6 Mana3 Manab4–GlcNAcb4–GlcNAc Mana2–Mana2–Mana3	2.3	5.5
D/M6.1 (6.1,7.1)	Mana6 Mana6 Mana3 Manb4–GlcNAcb4–GlcNAc Mana2–Mana2–Mana3	4.7	13.4

FIG.33A

Peak/code (G.U. ODS, amide)	PA–oligosaccharide structure	Secreted hTf (mol%) –GalT	Secreted hTf (mol%) +GalT
E1/M9.2 (6.3,10.3)	Mana2–Mana6 Mana6 Mana2–Mana3 Manb4–GlcNAcb4–GlcNAc Glca3–Mana2–Mana2–Mana3	1.3	3.7
E2/M8.2 (6.4,8.5)	Mana6 Mana6 Mana2–Mana3 Manb4–GlcNAcb4–GlcNAc Mana2–Mana2–Mana3	0.3	0.8
F1/M5.1 (7.2,6.2)	Mana6 Mana6 Mana3 Manb4–GlcNAcb4–GlcNAc Mana3	4.6	2.4
F2/000.1 (7.4,4.3)	Mana6 Manb4–GlcNAcb4–GlcNAc Mana3	9.0	5.8
F3/100.2 (7.4,4.7)	Mana6 Manb4–GlcNAcb4–GlcNAc GlcNAcb2–Mana3	6.5	3.1
G1/M6.10 (7.9,6.8)	Mana6 Mana6 Mana2–Mana3 Manb4–GlcNAcb4–GlcNAc Mana3	1.1	1.1

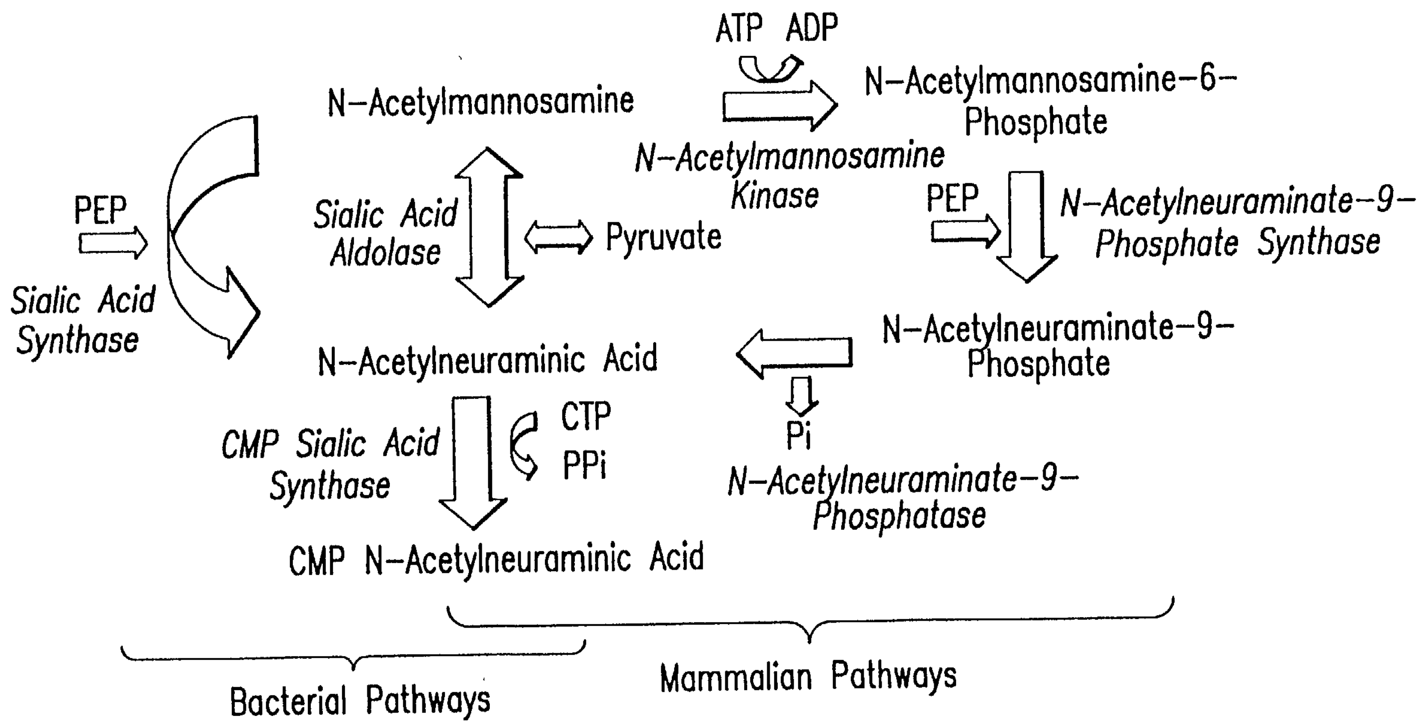
FIG.33B

Peak/code (G.U. ODS, amide)	PA-oligosaccharide structure	Secreted hTf (mol%) −GalT	Secreted hTf (mol%) +GalT
G2/100.4 (8.0,5.7)	Mana6 Manb4−GlcNAcb4−GlcNAc Galb4−GlcNAcb2−Mana3	nd	5.0
H/000.1FF (8.5,5.5)	Fuca 6 Mana6 Manb4−GlcNAcb4−GlcNAc Mana3 Fuca 3	5.9	1.7
I/100.4FF (8.9,7.0)	Fuca 6 Mana6 Manb4−GlcNAcb4−GlcNAc Galb4−GlcNAcb2−Mana3 Fuca 3	nd	1.3
J1/010.0 (7.2,6.2)	Fuca 6 Mana6 Manb4−GlcNAcb4−GlcNAc	23.4	4.0
J2/010.1 10.2,4.7)	Fuca 6 Mana6 Manb4−GlcNAcb4−GlcNAc Mana3	15.7	6.1

FIG.33C

Peak/code (G.U. ODS, amide)	PA–oligosaccharide structure	Secreted hTf (mol%) −GalT	Secreted hTf (mol%) +GalT
J3/110.2 (10.2,5.1)	Fuca 6 on GlcNAc (reducing end) Mana6 \ Manb4–GlcNAcb4–GlcNAc GlcNAcb2–Mana3 /	3.5	nd
K/110.4 (10.9,6.3)	Fuca 6 on GlcNAc (reducing end) Mana6 \ Manb4–GlcNAcb4–GlcNAc Galb4–GlcNAcb2–Mana3 /	nd	4.3
L/110.1 (12.7,5.1)	Fuca 6 on GlcNAc (reducing end) GlcNAcb2–Mana6 \ Manb4–GlcNAcb4–GlcNAc Mana3 /	3.9	0.7

FIG.33D



ATP ADP
N–Acetylmannosamine
N–Acetylmannosamine–6–Phosphate
N–Acetylmannosamine Kinase
PEP
Sialic Acid Synthase
Sialic Acid Aldolase
Pyruvate
PEP
N–Acetylneuraminate–9–Phosphate Synthase
N–Acetylneuraminate–9–Phosphate
N–Acetylneuraminic Acid
CMP Sialic Acid Synthase
CTP
PPi
Pi
N–Acetylneuraminate–9–Phosphatase
CMP N–Acetylneuraminic Acid
Bacterial Pathways
Mammalian Pathways

FIG.34

```
                10         20         30         40         50         60
                 .          .          .          .          .          .
  1 CGG ACC CAG ACT GGT AGT GCA GGC TTT GGA CCC CGA GCC GCT GCA ATG CCG CTG GAG CTG 60
  1                                                             M   P   L   E   L  5
                70         80         90        100        110        120
                 .          .          .          .          .          .
 61 GAG CTG TGT CCC GGG CGC TGG GTG GGC GGG CAA CAC CCG TGC TTC ATC ATT GCC GAG ATC 120
  6  E   L   C   P   G   R   W   V   G   G   Q   H   P   C   F   I   I   A   E   I  25
               130        140        150        160        170        180
                 .          .          .          .          .          .
121 GGC CAG AAC CAC CAG GGC GAC CTG GAC GTA GCC AAG CGC ATG ATC CGC ATG GCC AAG GAG 180
 26  G   Q   N   H   Q   G   D   L   D   V   A   K   R   M   I   R   M   A   K   E  45
               190        200        210        220        230        240
                 .          .          .          .          .          .
181 TGT GGG GCT GAT TGT GCC AAG TTC CAG AAG AGT GAG CTA GAA TTC AAG TTT AAT CGG AAA 240
 46  C   G   A   D   C   A   K   F   Q   K   S   E   L   E   F   K   F   N   R   K  65
               250        260        270        280        290        300
                 .          .          .          .          .          .
241 GCC TTG GAG AGG CCA TAC ACC TCG AAG CAT TCC TGG GGG AAG ACG TAC GGG GAG CAC AAA 300
 66  A   L   E   R   P   Y   T   S   K   H   S   W   G   K   T   Y   G   E   H   K  85
               310        320        330        340        350        360
                 .          .          .          .          .          .
301 CGA CAT CTG GAG TTC AGC CAT GAC CAG TAC AGG GAG CTG CAG AGG TAC GCC GAG GAG GTT 360
 86  R   H   L   E   F   S   H   D   Q   Y   R   E   L   Q   R   Y   A   E   E   V  105
               370        380        390        400        410        420
                 .          .          .          .          .          .
361 GGG ATC TTC TTC ACT GCC TCT GGC ATG GAT GAG ATG GCA GTT GAA TTC CTG CAT GAA CTG 420
106  G   I   F   F   T   A   S   G   M   D   E   M   A   V   E   F   L   H   E   L  125
               430        440        450        460        470        480
                 .          .          .          .          .          .
421 AAT GTT CCA TTT TTC AAA GTT GGA TCT GGA GAC ACT AAT AAT TTT CCT TAT CTG GAA AAG 480
126  N   V   P   F   F   K   V   G   S   G   D   T   N   N   F   P   Y   L   E   K  145
```

FIG. 35A

```
               490       500       510       520       530       540
481 ACA GCC AAA AAA GGT CGC CCA ATG GTG ATC TCC AGT GGG ATG CAG TCA ATG GAC ACC ATG 540
146  T   A   K   K   G   R   P   M   V   I   S   S   G   M   Q   S   M   D   T   M  165
               550       560       570       580       590       600
541 AAG CAA GTT TAT CAG ATC GTG AAG CCC CTC AAC CCC AAC TTC TGC TTC TTG CAG TGT ACC 600
166  K   Q   V   Y   Q   I   V   K   P   L   N   P   N   F   C   F   L   Q   C   T  185
               610       620       630       640       650       660
601 AGC GCA TAC CCG CTC CAG CCT GAG GAC GTC AAC CTG CGG GTC ATC TCG GAA TAT CAG AAG 660
186  S   A   Y   P   L   Q   P   E   D   V   N   L   R   V   I   S   E   Y   Q   K  205
               670       680       690       700       710       720
661 CTC TTT CCT GAC ATT CCC ATA GGG TAT TCT GGG CAT GAA ACA GGC ATA GCG ATA TCT GTG 720
206  L   F   P   D   I   P   I   G   Y   S   G   H   E   T   G   I   A   I   S   V  225
               730       740       750       760       770       780
721 GCC GCA GTG GCT CTG GGG GCC AAG GTG TTG GAA CGT CAC ATA ACT TTG GAC AAG ACC TGG 780
226  A   A   V   A   L   G   A   K   V   L   E   R   H   I   T   L   D   K   T   W  245
               790       800       810       820       830       840
781 AAG GGG AGT GAC CAC TCG GCC TCG CTG GAG CCT GGA GAA CTG GCC GAG CTG GTG CGG TCA 840
246  K   G   S   D   H   S   A   S   L   E   P   G   E   L   A   E   L   V   R   S  265
               850       860       870       880       890       900
841 GTG CGT CTT GTG GAG CGT GCC CTG GGC TCC CCA ACC AAG CAG CTG CTG CCC TGT GAG ATG 900
266  V   R   L   V   E   R   A   L   G   S   P   T   K   Q   L   L   P   C   E   M  285
               910       920       930       940       950       960
901 GCC TGC AAT GAG AAG CTG GGC AAG TCT GTG GTG GCC AAA GTG AAA ATT CCG GAA GGC ACC 960
286  A   C   N   E   K   L   G   K   S   V   V   A   K   V   K   I   P   E   G   T  305
```

FIG. 35B

```
                970         980         990         1000        1010        1020
                  .           .           .           .           .           .
 961 ATT CTA ACA ATG GAC ATG CTC ACC GTG AAG GTG GGT GAG CCC AAA GCC TAT CCT CCT GAA 1020
 306  I   L   T   M   D   M   L   T   V   K   V   G   E   P   K   A   Y   P   P   E  325
                1030        1040        1050        1060        1070        1080
                  .           .           .           .           .           .
1021 GAC ATC TTT AAT CTA GTG GGC AAG AAG GTC CTG GTC ACT GTT GAA GAG GAT GAC ACC ATC 1080
 326  D   I   F   N   L   V   G   K   K   V   L   V   T   V   E   E   D   D   T   I  345
                1090        1100        1110        1120        1130        1140
                  .           .           .           .           .           .
1081 ATG GAA GAA TTG GTA GAT AAT CAT GGC AAA AAA ATC AAG TCT TAA AAA TAA AGT GCC ATT 1140
 346  M   E   E   L   V   D   N   H   G   K   K   I   K   S   *                      359

1141 CTC TGA 1146
```

FIG. 35C

```
  1 MPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVAKRMIRMAKECGADCAKFQKSELEF
    |                   | |||| || |  | |  ||  ||| |    |||
  1 MS---------------NIYIVAEIGCNHNGSVDIAREMILKAKEAGVNAVKFQTFKADK

 61 KFNRKALERPYTSKHSWG-KTYGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAV
         |    |  |         |    ||   | |  |  ||            ||
 46 LISAIAPKAEYQIKNTGELESQLEMTKKLEMKYDDYLHLMEYAVSLNLDVFSTPFDEDSI

120 EFLHELNVPFFKVGSGDTNNFPYLEKTAK---KGRPMVISSGMQSMDTMKQ---VYQIVK
     ||  |     |  ||   | ||||| ||         || ||   |  ||        |
106 DFLASLKQKIWKIPSGELLNLPYLEKIAKLPIPDKKIIISTGMATIDEIKQSVSIFINNK

174 PLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIPIGYSGHETGIAISVAAVALGAK
        |   | |   ||   |||||  |    | ||   || | |  |     |||  |
166 VPVGNITILHCNTEYPTPFEDVNLNAINDLKKHFPKNNIGFSDHSSGFYAAIAAVPYGIT

234 VLERHITLDKTWKGSDHSASLEPGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGK
      | | ||||   | || || || ||  |   || ||  |||  |     |        |
226 FIEKHFTLDKSMSGPDHLASIEPDELKHLCIGVRCVEKSLGSNSKVVTASERKNKIVARK

294 SVVAKVKIPEGTILTMDMLTVKVGEPKAYPPEDIFNLVGKKVLVTVEEDDTIMEELVDNH
    |  ||  |  |        | |        |    || ||       | | |  ||
286 SIIAKTEIKKGEVFSEKNITTKRP-GNGISPMEWYNLLGK-----IAEQDFIPDELIIHS

354 G-KKIKS
      |
340 EFKNQGE
```

FIG. 35D

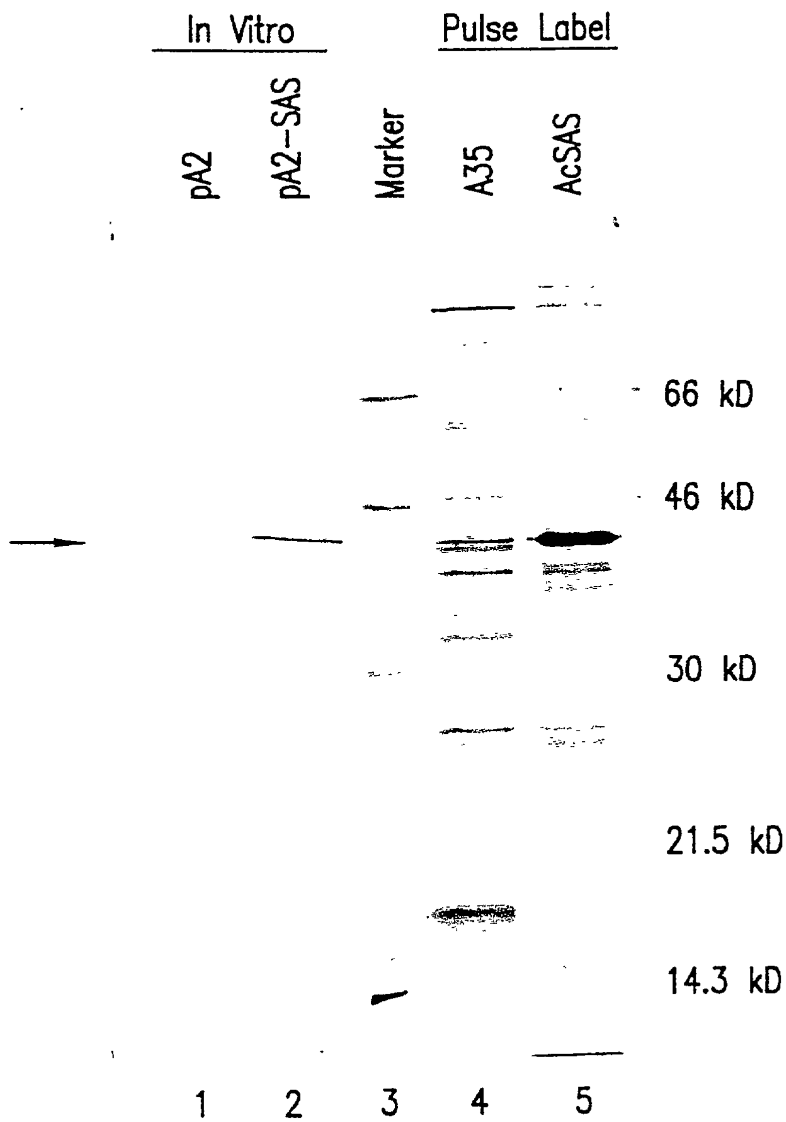

In Vitro
Pulse Label
pA2
pA2–SAS
Marker
A35
AcSAS
66 kD
46 kD
30 kD
21.5 kD
14.3 kD
1
2
3
4
5

FIG.36A

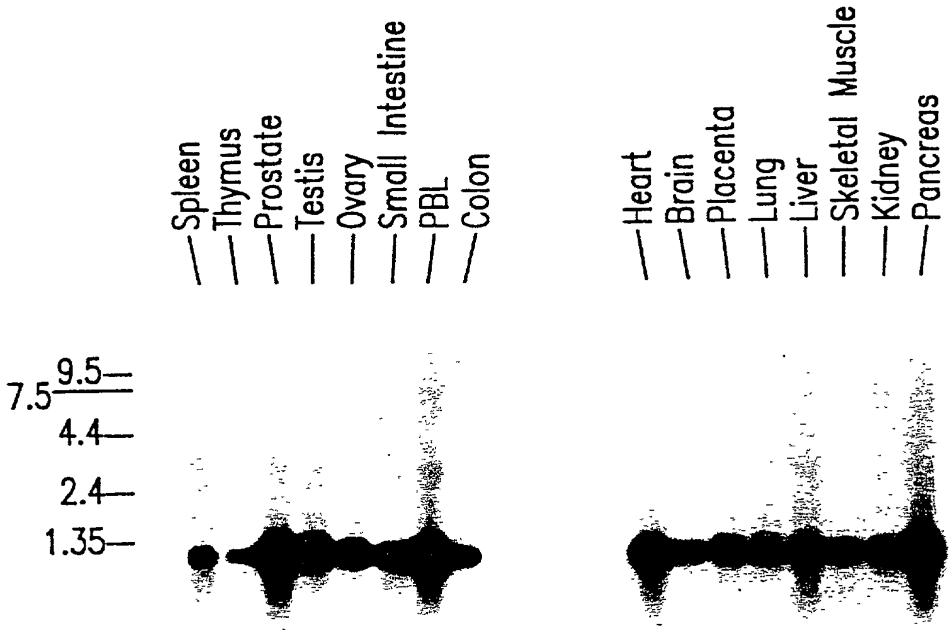
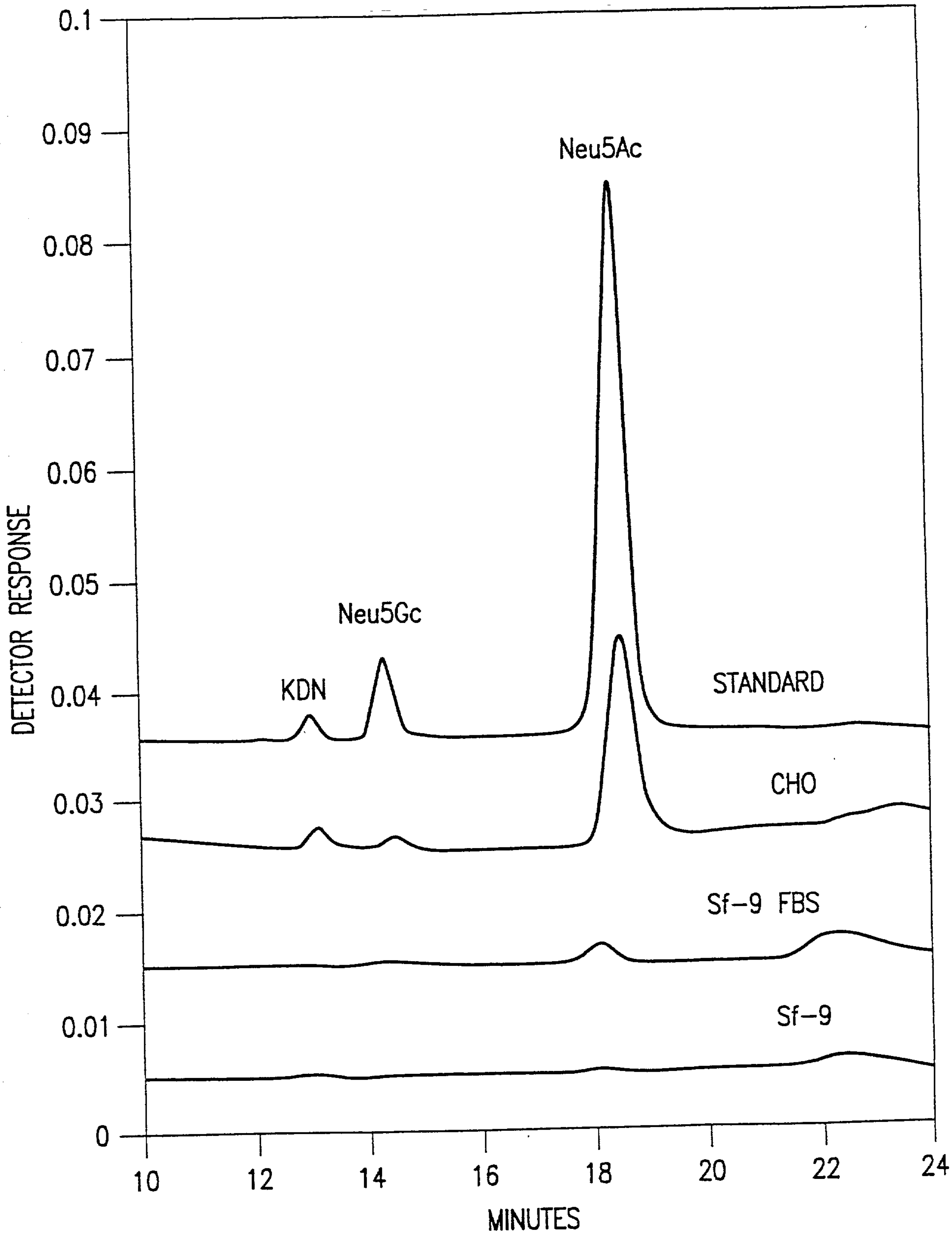

Spleen
Thymus
Prostate
Testis
Ovary
Small Intestine
PBL
Colon
Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
9.5
7.5
4.4
2.4
1.35

FIG.36B



0.1
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
DETECTOR RESPONSE
Neu5Ac
Neu5Gc
KDN
STANDARD
CHO
Sf-9 FBS
Sf-9
10
12
14
16
18
20
22
24
MINUTES

FIG. 37A

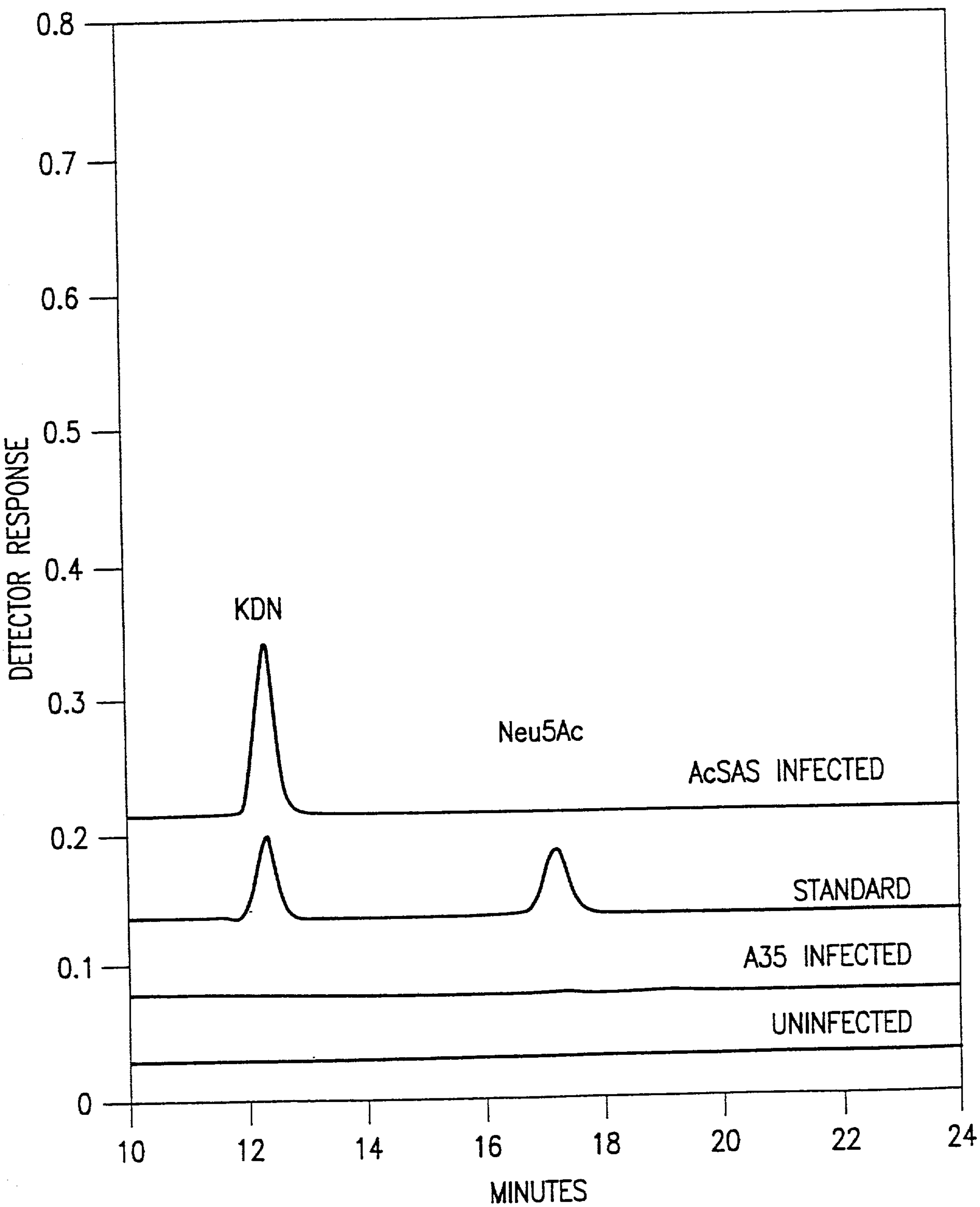

0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
DETECTOR RESPONSE
KDN
Neu5Ac
AcSAS INFECTED
STANDARD
A35 INFECTED
UNINFECTED
10
12
14
16
18
20
22
24
MINUTES

FIG. 37B

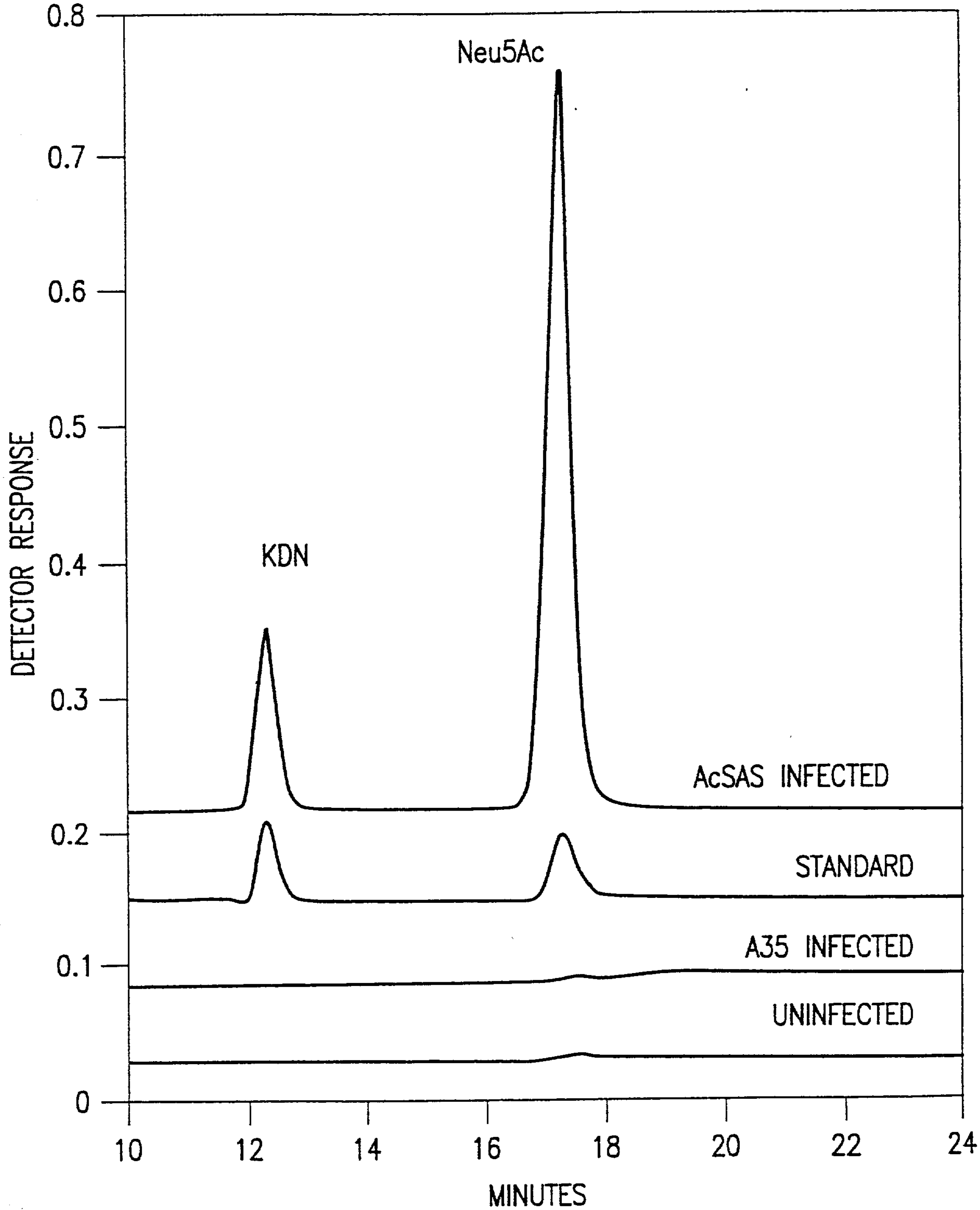

Neu5Ac
KDN
DETECTOR RESPONSE
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
AcSAS INFECTED
STANDARD
A35 INFECTED
UNINFECTED
10
12
14
16
18
20
22
24
MINUTES

FIG. 37C

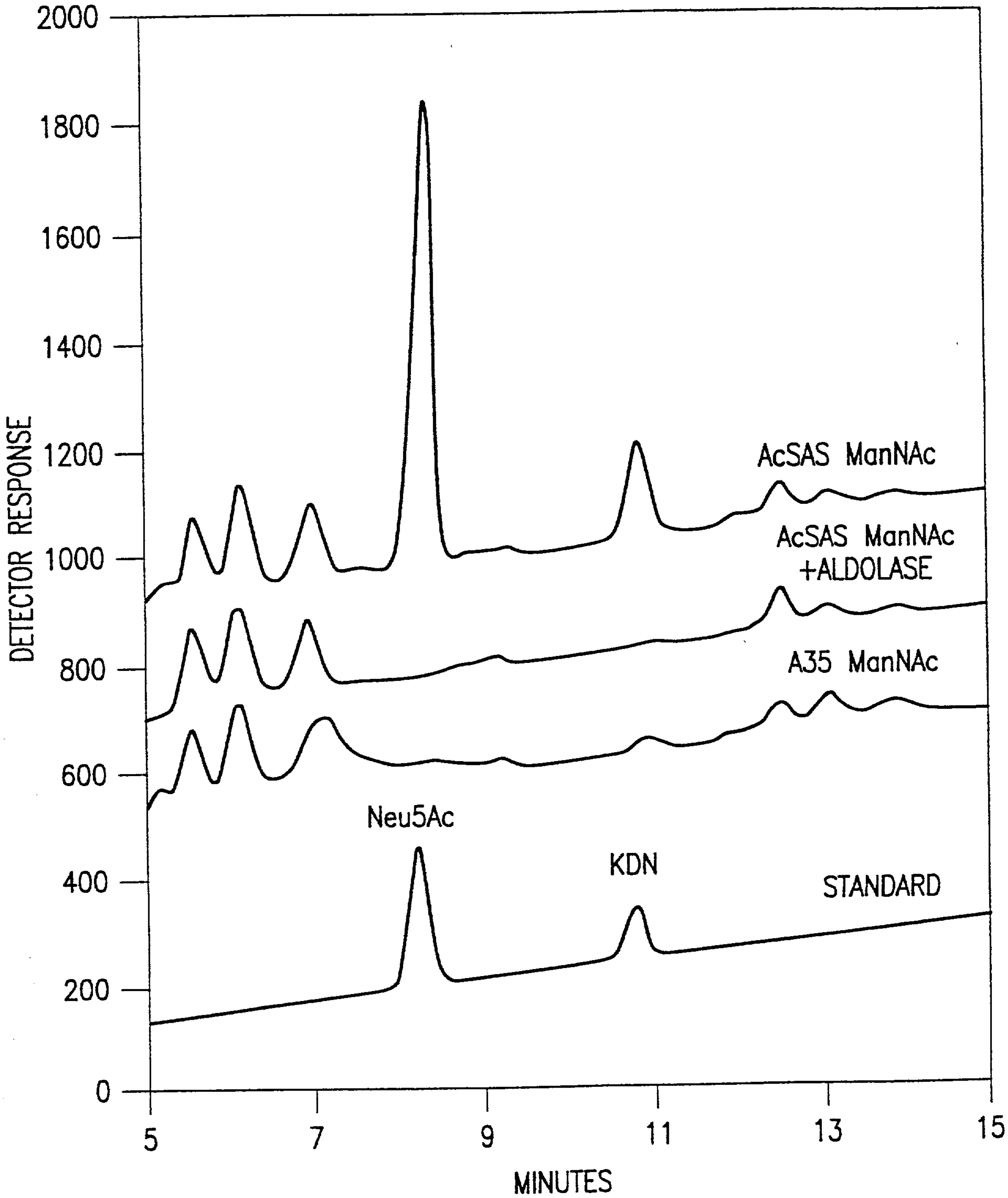
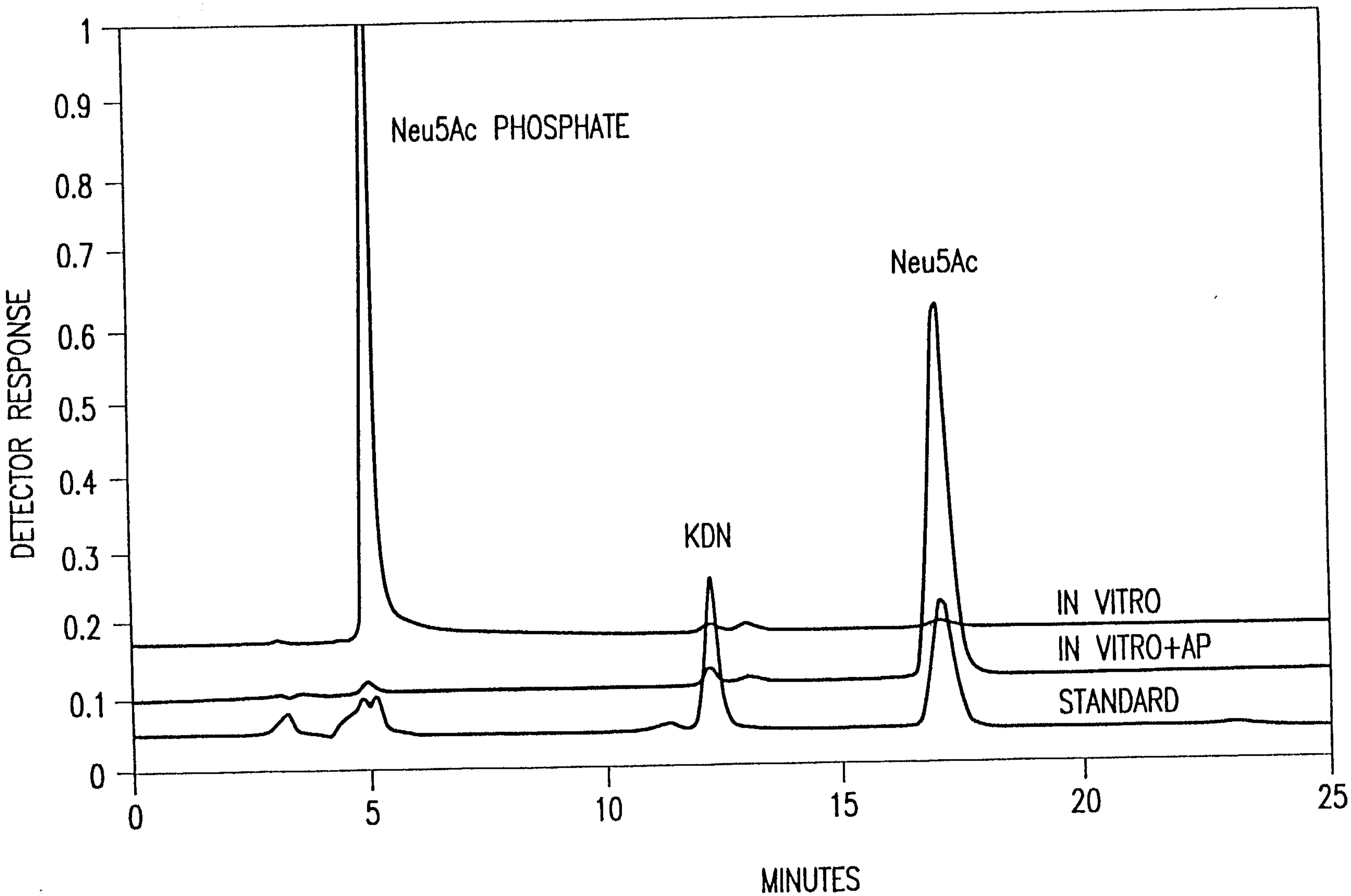

2000
1800
1600
1400
1200
1000
800
600
400
200
0
DETECTOR RESPONSE
AcSAS ManNAc
AcSAS ManNAc
+ALDOLASE
A35 ManNAc
Neu5Ac
KDN
STANDARD
5
7
9
11
13
15
MINUTES

FIG. 37D



Neu5Ac PHOSPHATE
KDN
Neu5Ac
IN VITRO
IN VITRO+AP
STANDARD
DETECTOR RESPONSE
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
5
10
15
20
25
MINUTES

FIG. 38A

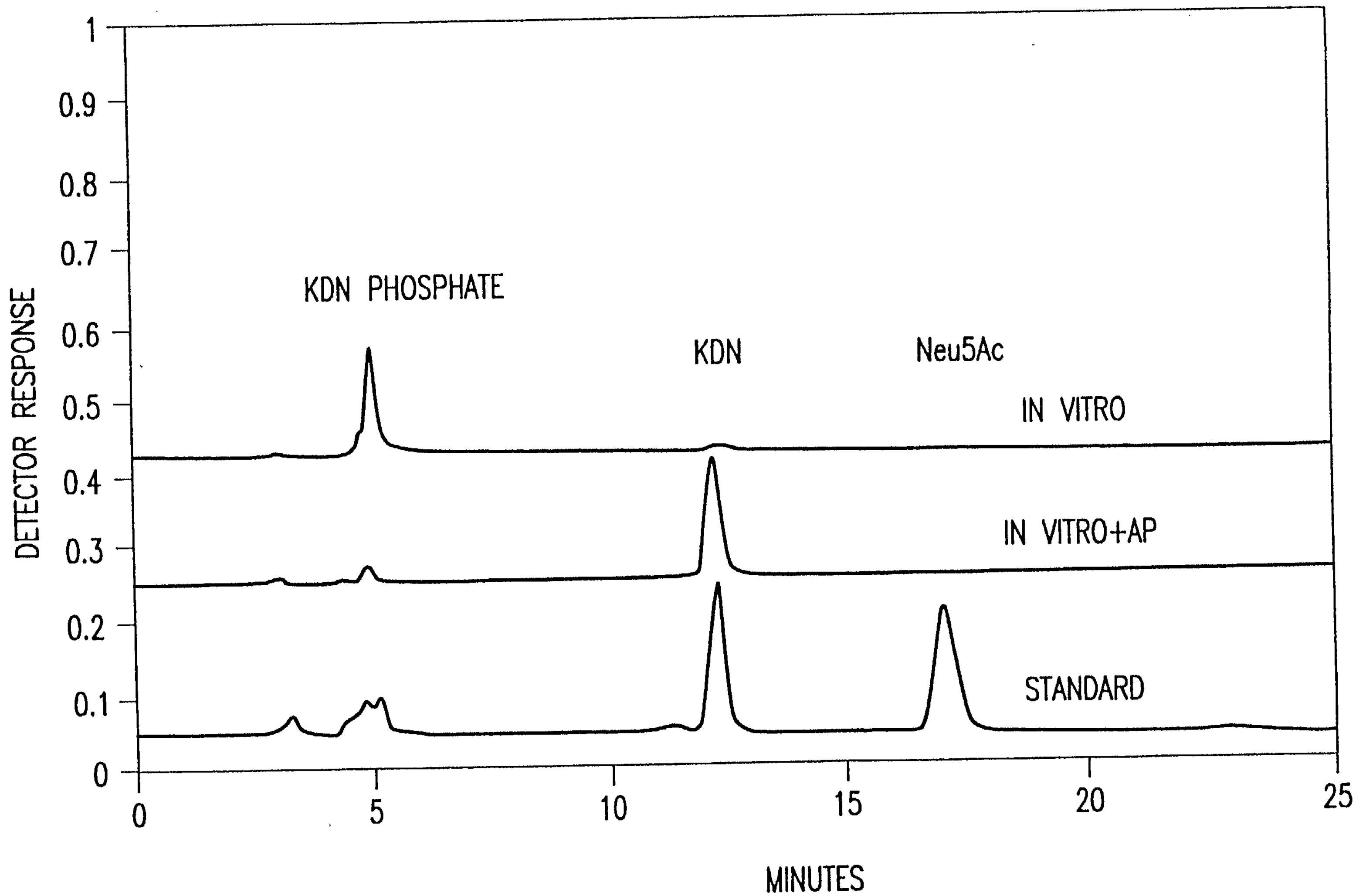
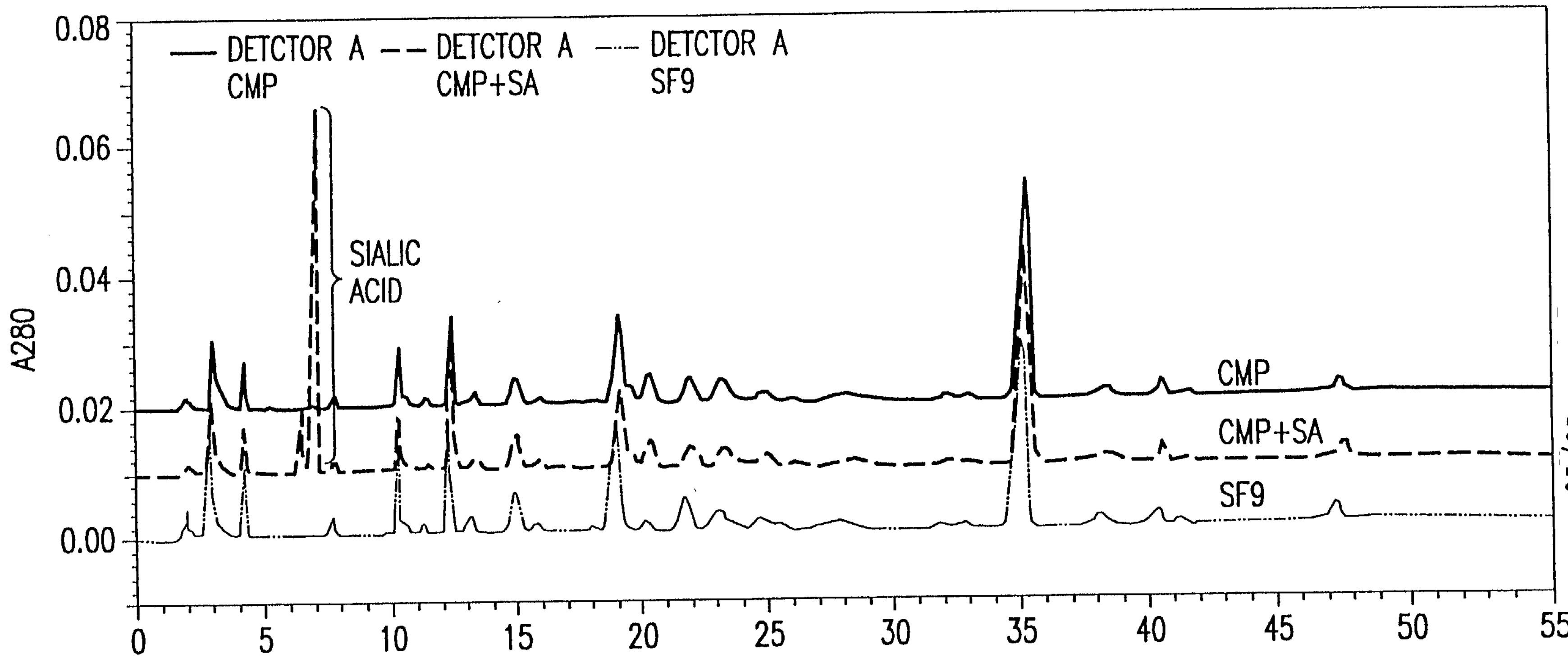

DETECTOR RESPONSE
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
KDN PHOSPHATE
KDN
Neu5Ac
IN VITRO
IN VITRO+AP
STANDARD
0
5
10
15
20
25
MINUTES

FIG. 38B



DETCTOR A CMP
DETCTOR A CMP+SA
DETCTOR A SF9
SIALIC ACID
CMP
CMP+SA
SF9
A280
0.08
0.06
0.04
0.02
0.00
0
5
10
15
20
25
30
35
40
45
50
55
MINUTES

FIG. 39